FIGURE 1

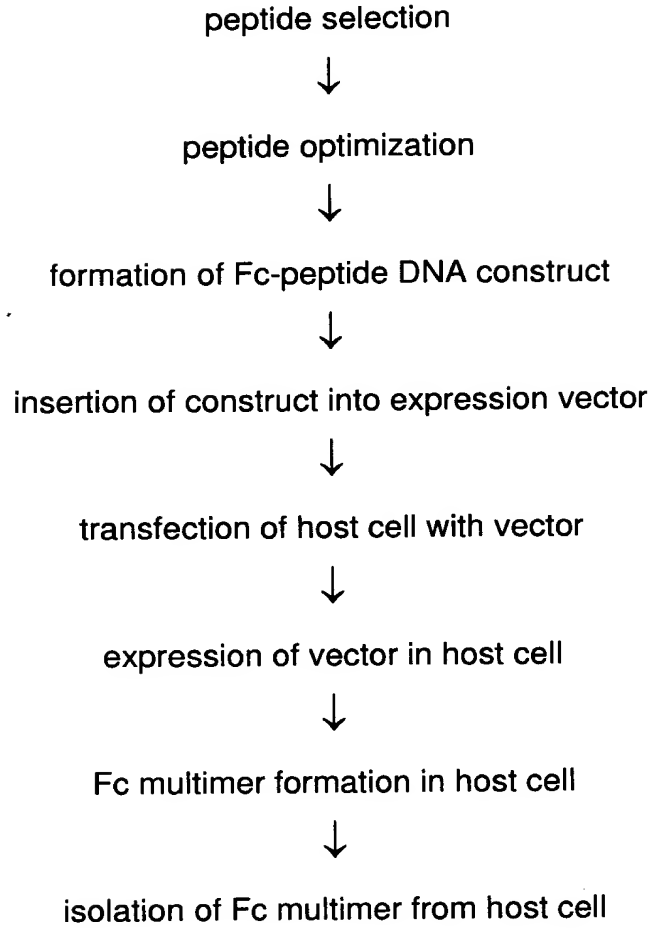

peptide selection
peptide optimization
formation of Fc-peptide DNA construct
insertion of construct into expression vector
transfection of host cell with vector
expression of vector in host cell
Fc multimer formation in host cell
isolation of Fc multimer from host cell

FIGURE 2

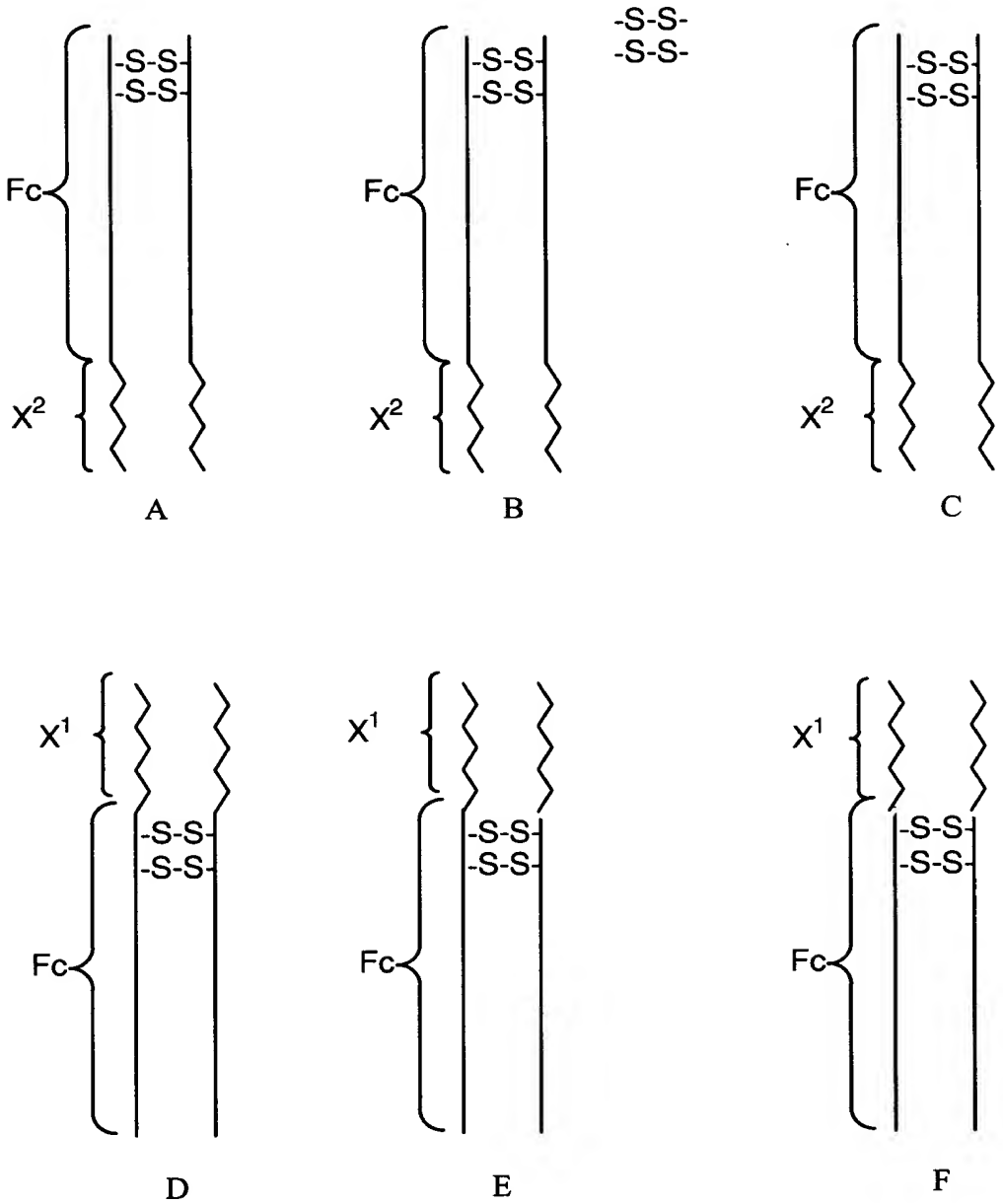


FIGURE 3

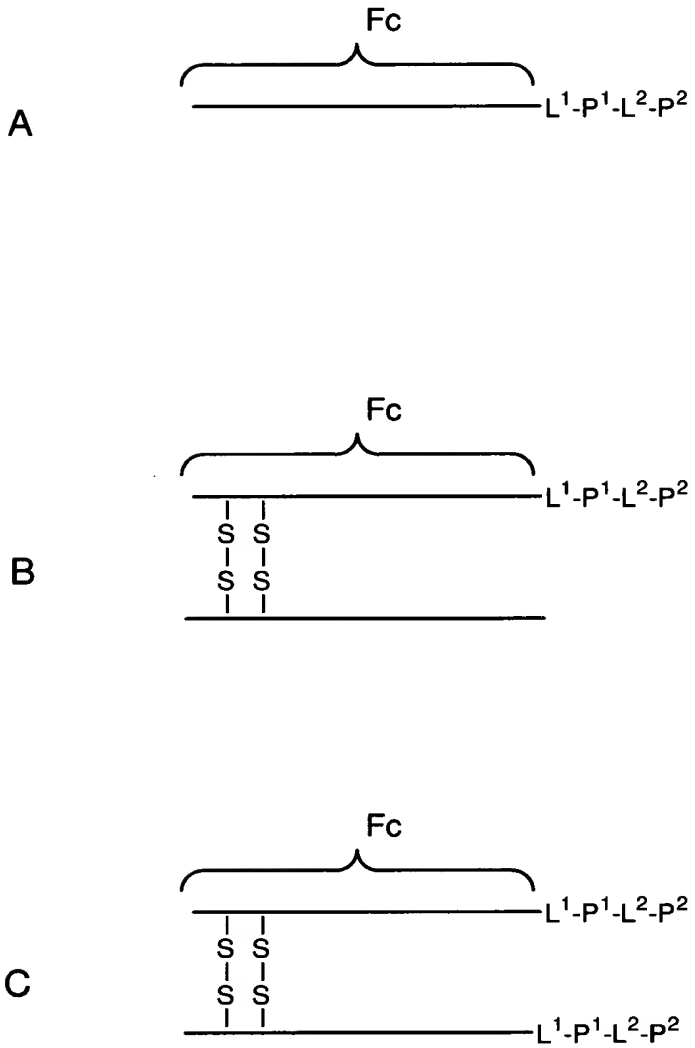
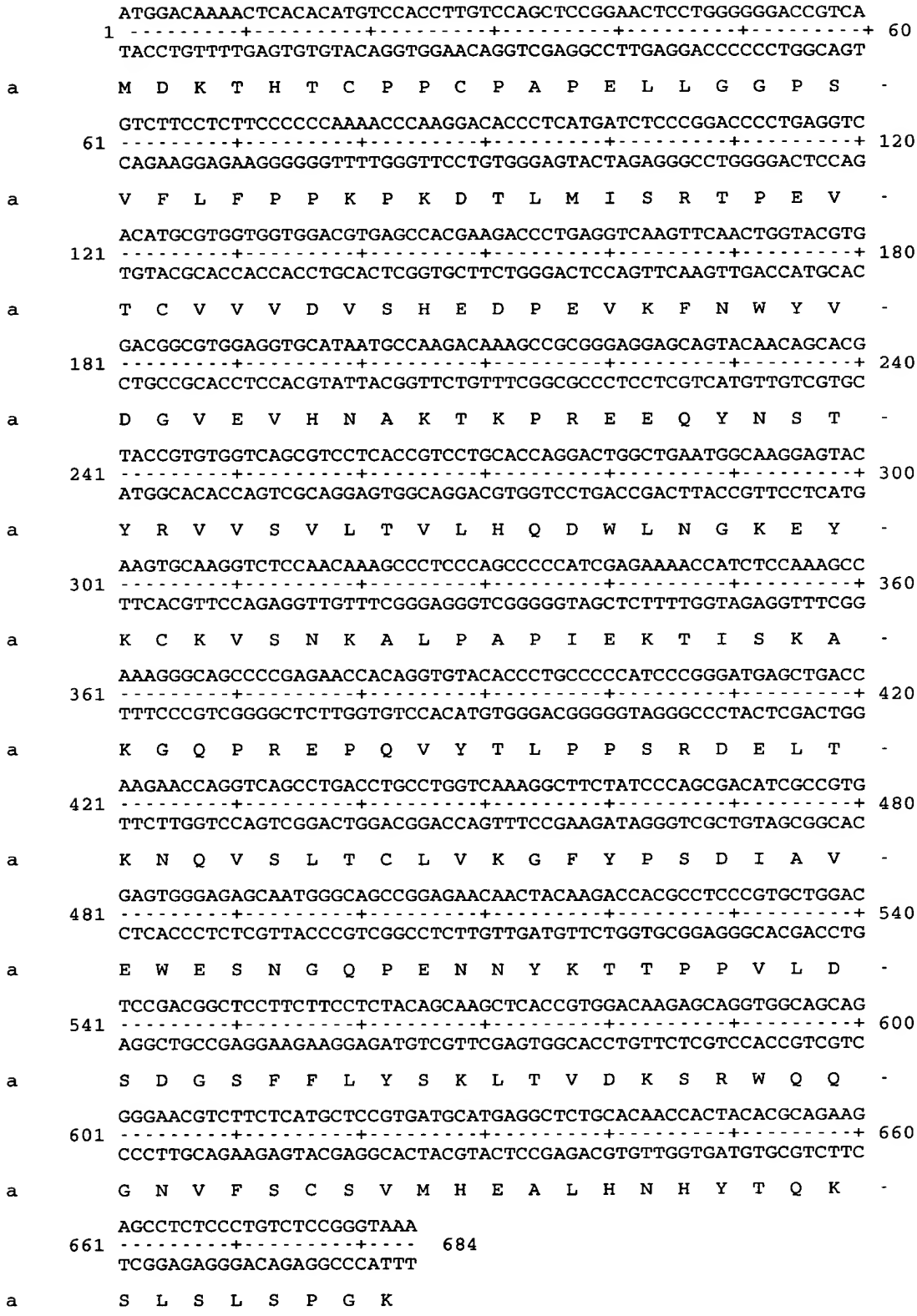


FIGURE 4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a M D K T H T C P P C P A P E L L G G P S -
GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC
61 ---------+---------+---------+---------+---------+---------+ 120
CAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG
a V F L F P P K P K D T L M I S R T P E V -
ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
121 ---------+---------+---------+---------+---------+---------+ 180
TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC
a T C V V V D V S H E D P E V K F N W Y V -
GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
181 ---------+---------+---------+---------+---------+---------+ 240
CTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGC
a D G V E V H N A K T K P R E E Q Y N S T -
TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
241 ---------+---------+---------+---------+---------+---------+ 300
ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATG
a Y R V V S V L T V L H Q D W L N G K E Y -
AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
301 ---------+---------+---------+---------+---------+---------+ 360
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a K C K V S N K A L P A P I E K T I S K A -
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC
361 ---------+---------+---------+---------+---------+---------+ 420
TTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGG
a K G Q P R E P Q V Y T L P P S R D E L T -
AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG
421 ---------+---------+---------+---------+---------+---------+ 480
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a K N Q V S L T C L V K G F Y P S D I A V -
GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC
481 ---------+---------+---------+---------+---------+---------+ 540
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a E W E S N G Q P E N N Y K T T P P V L D -
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541 ---------+---------+---------+---------+---------+---------+ 600
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a S D G S F F L Y S K L T V D K S R W Q Q -
GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG
601 ---------+---------+---------+---------+---------+---------+ 660
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a G N V F S C S V M H E A L H N H Y T Q K -
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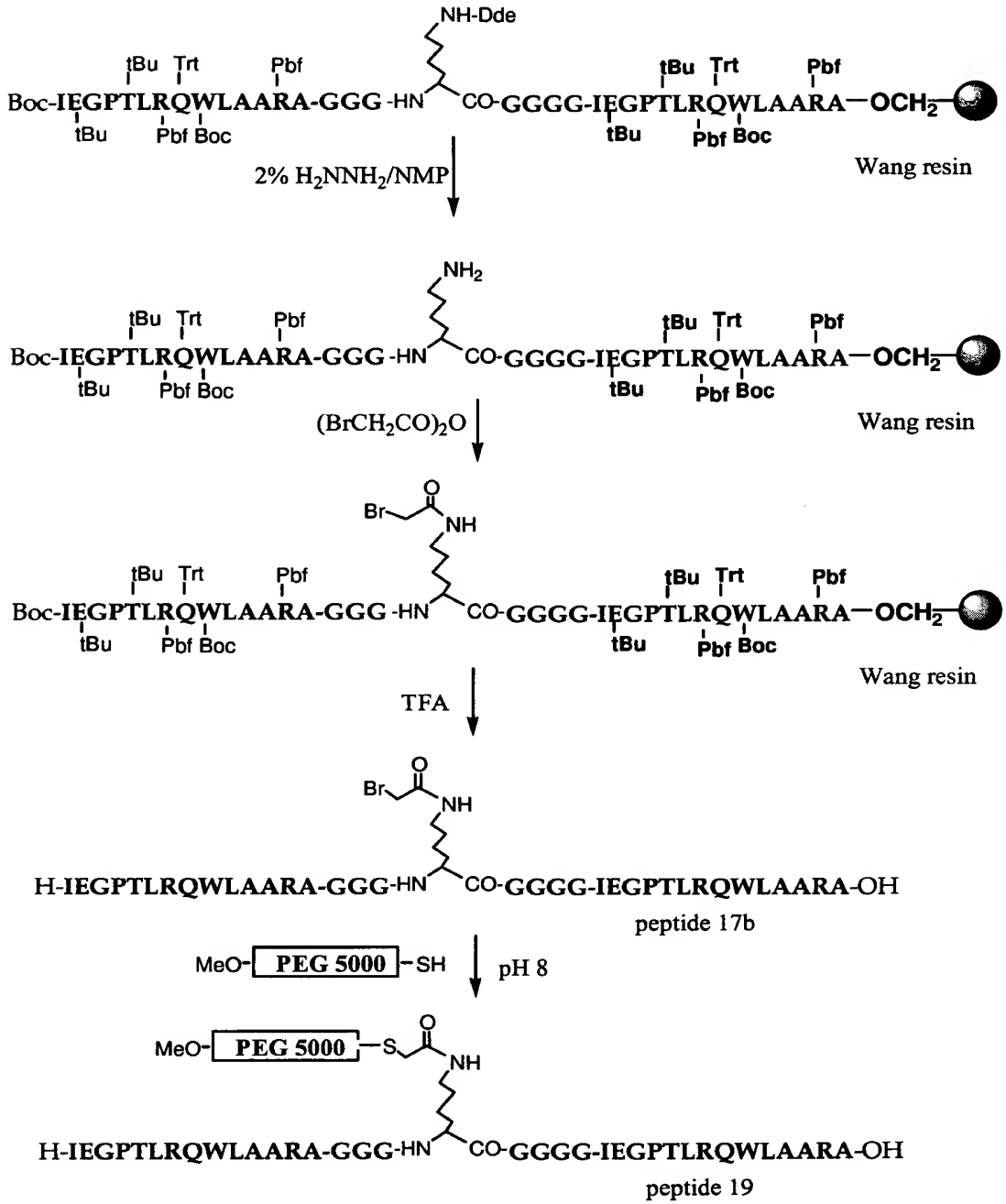
a S L S L S P G K

FIGURE 5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CO-GGGG-IEGPTLRQWLAARA—OCH2—
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tBu Pbf Boc
Wang resin
2% H2NNH2/NMP
NH2
(BrCH2CO)2O
Br
O
NH
TFA
H-IEGPTLRQWLAARA-GGG-HN
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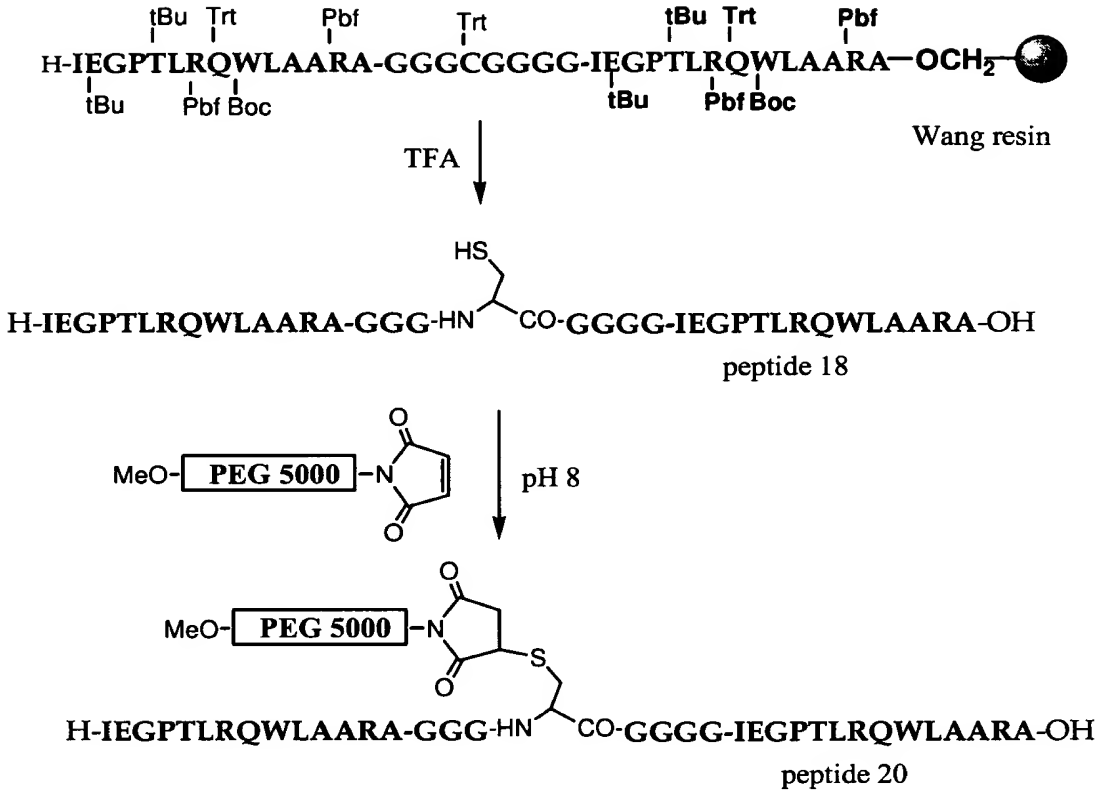
peptide 17b
MeO-PEG 5000-SH
pH 8
MeO-PEG 5000-S
peptide 19

FIGURE 6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Wang resin
TFA
HS
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peptide 18
MeO- PEG 5000 -N
pH 8
MeO- PEG 5000 -N
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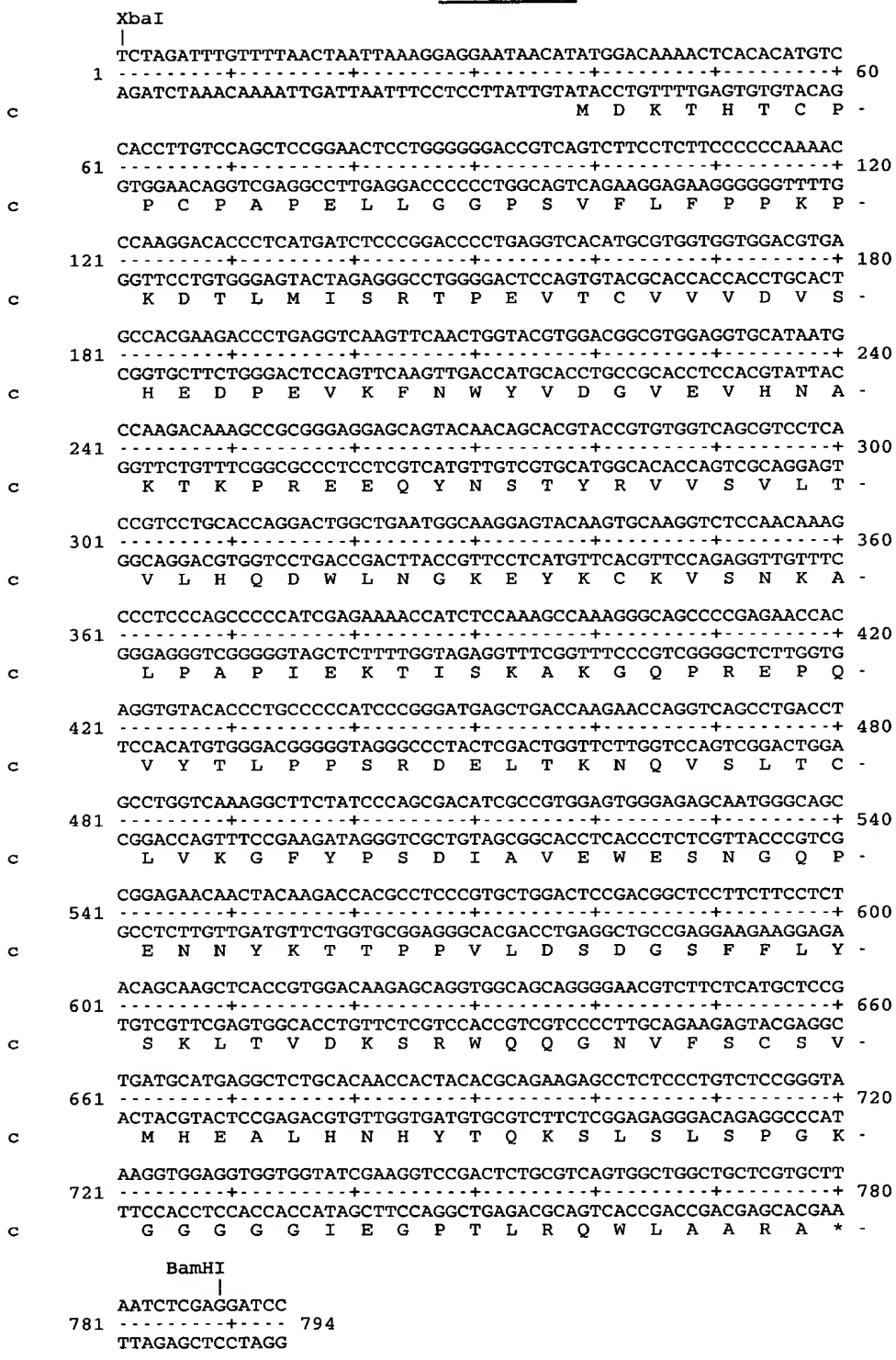
peptide 20

FIGURE 7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V Y T L P P S R D E L T K N Q V S L T C
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E N N Y K T T P P V L D S D G S F F L Y
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S K L T V D K S R W Q Q G N V F S C S V
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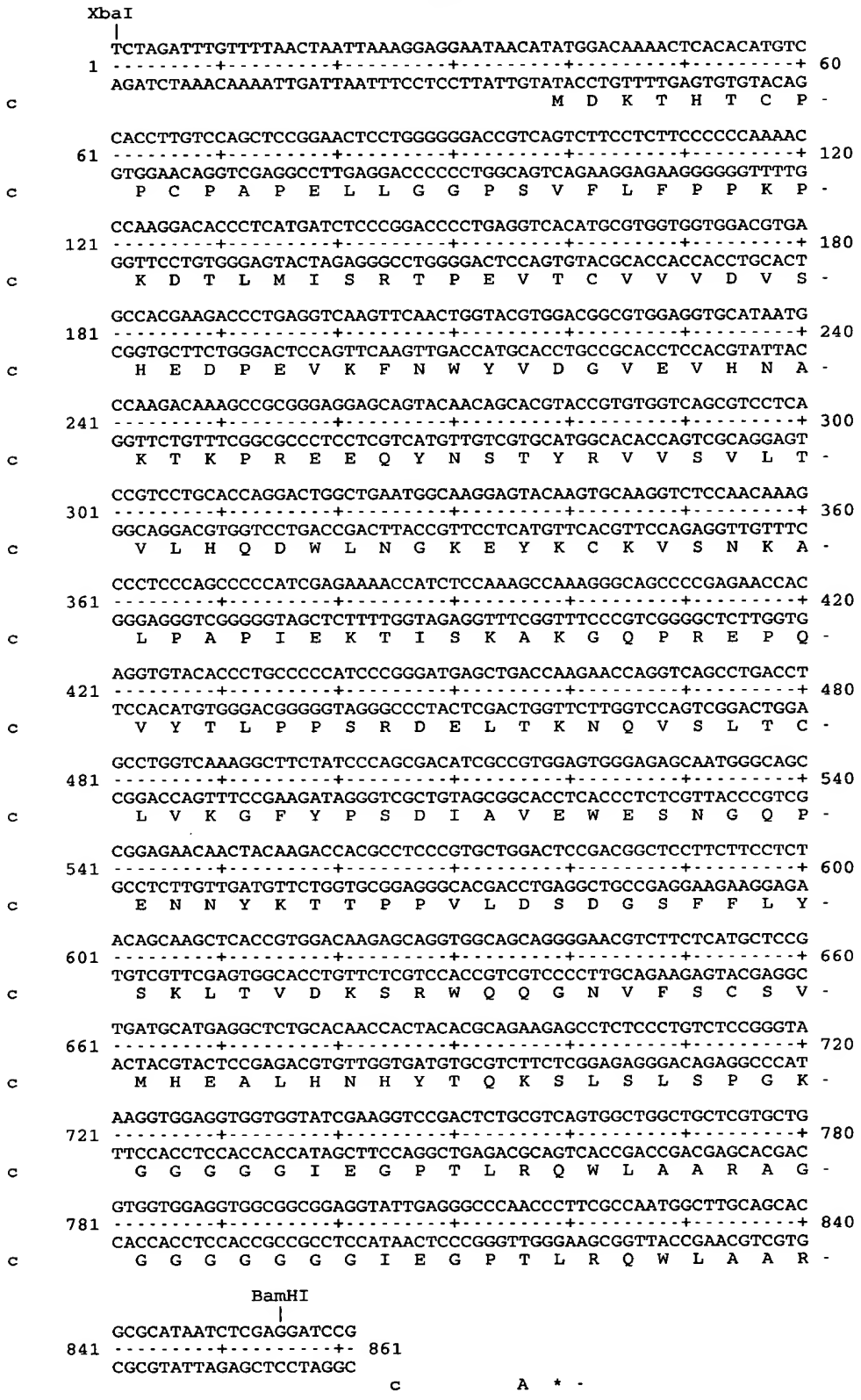
794

FIGURE 8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K T K P R E E Q Y N S T Y R V V S V L T
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V L H Q D W L N G K E Y K C K V S N K A
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L P A P I E K T I S K A K G Q P R E P Q
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V Y T L P P S R D E L T K N Q V S L T C
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S K L T V D K S R W Q Q G N V F S C S V
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BamHI
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CGCGTATTAGAGCTCCTAGGC
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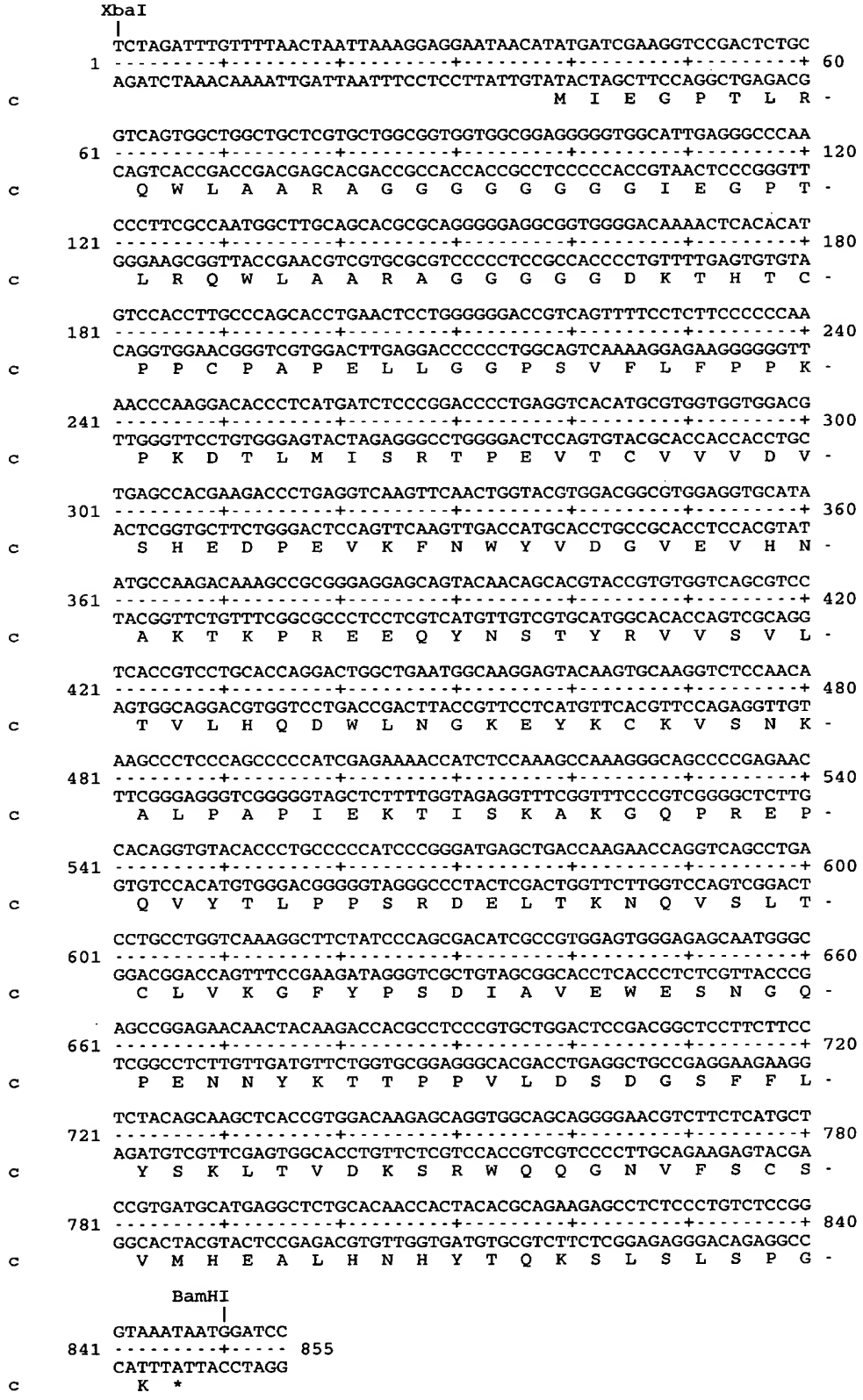
FIGURE 9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c Q W L A A R A G G G G G G G G I E G P T -
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GGGAAGCGGTTACCGAACGTCGTGCGCGTCCCCCTCCGCCACCCCTGTTTTGAGTGTGTA
c L R Q W L A A R A G G G G G D K T H T C -
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CAGGTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAAAAGGAGAAGGGGGGTT
c P P C P A P E L L G G P S V F L F P P K -
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c P K D T L M I S R T P E V T C V V V D V -
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ACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTAT
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c A K T K P R E E Q Y N S T Y R V V S V L -
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c T V L H Q D W L N G K E Y K C K V S N K -
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c A L P A P I E K T I S K A K G Q P R E P -
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GTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACT
c Q V Y T L P P S R D E L T K N Q V S L T -
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c C L V K G F Y P S D I A V E W E S N G Q -
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c P E N N Y K T T P P V L D S D G S F F L -
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c Y S K L T V D K S R W Q Q G N V F S C S -
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GGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCC
c V M H E A L H N H Y T Q K S L S L S P G -
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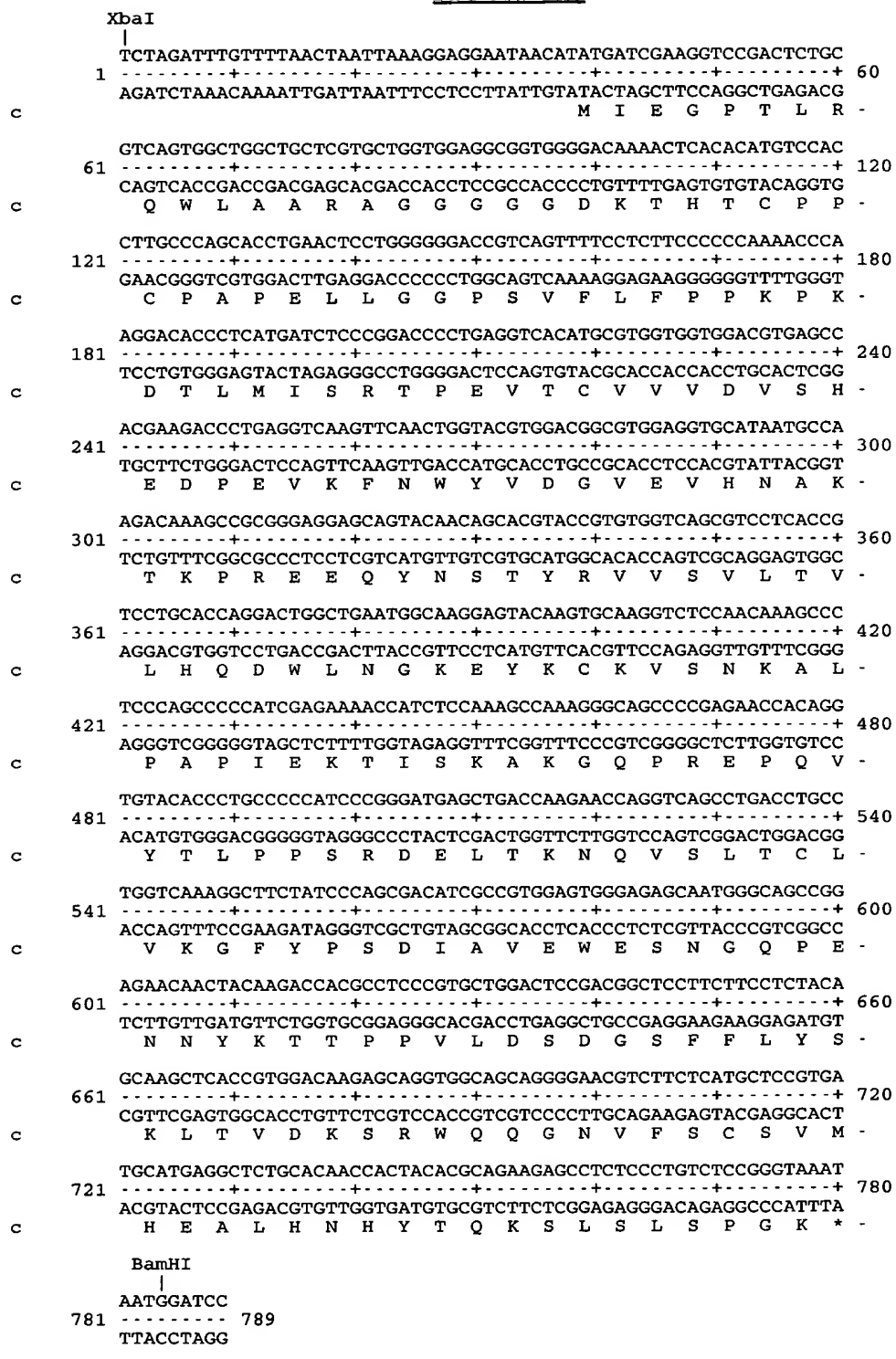
GTAAATAATGGATCC
841 ---------+----- 855
CATTTATTACCTAGG
c K *

FIGURE 10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c Q W L A A R A G G G G G D K T H T C P P -
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c C P A P E L L G G P S V F L F P P K P K -
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c D T L M I S R T P E V T C V V V D V S H -
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c Y T L P P S R D E L T K N Q V S L T C L -
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781 --------- 789
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FIGURE 11

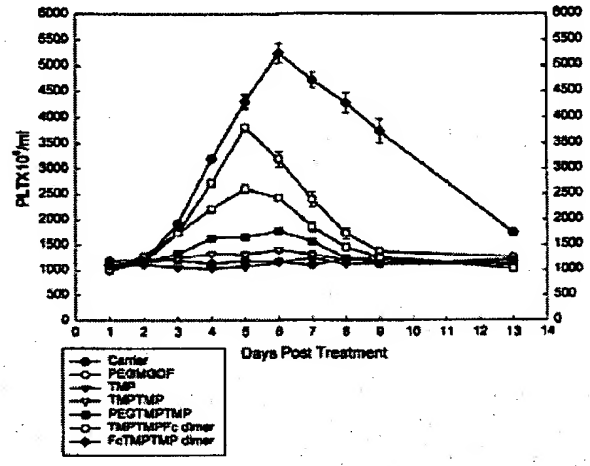

PLTX10³/ml
Days Post Treatment
Carrier
PEGMGDF
TMPI
TMPTMP
PEGTMPTMP
TMPTMPFc dimer
FcTMPTMP dimer

FIGURE 12

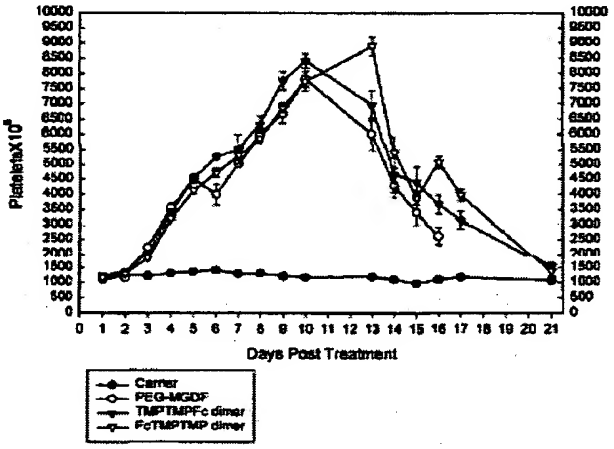

Platelets X10³
Days Post Treatment
Carrier
PEG-MGDF
TMPTMPFc dimer
FcTMPTMP dimer

FIGURE 13

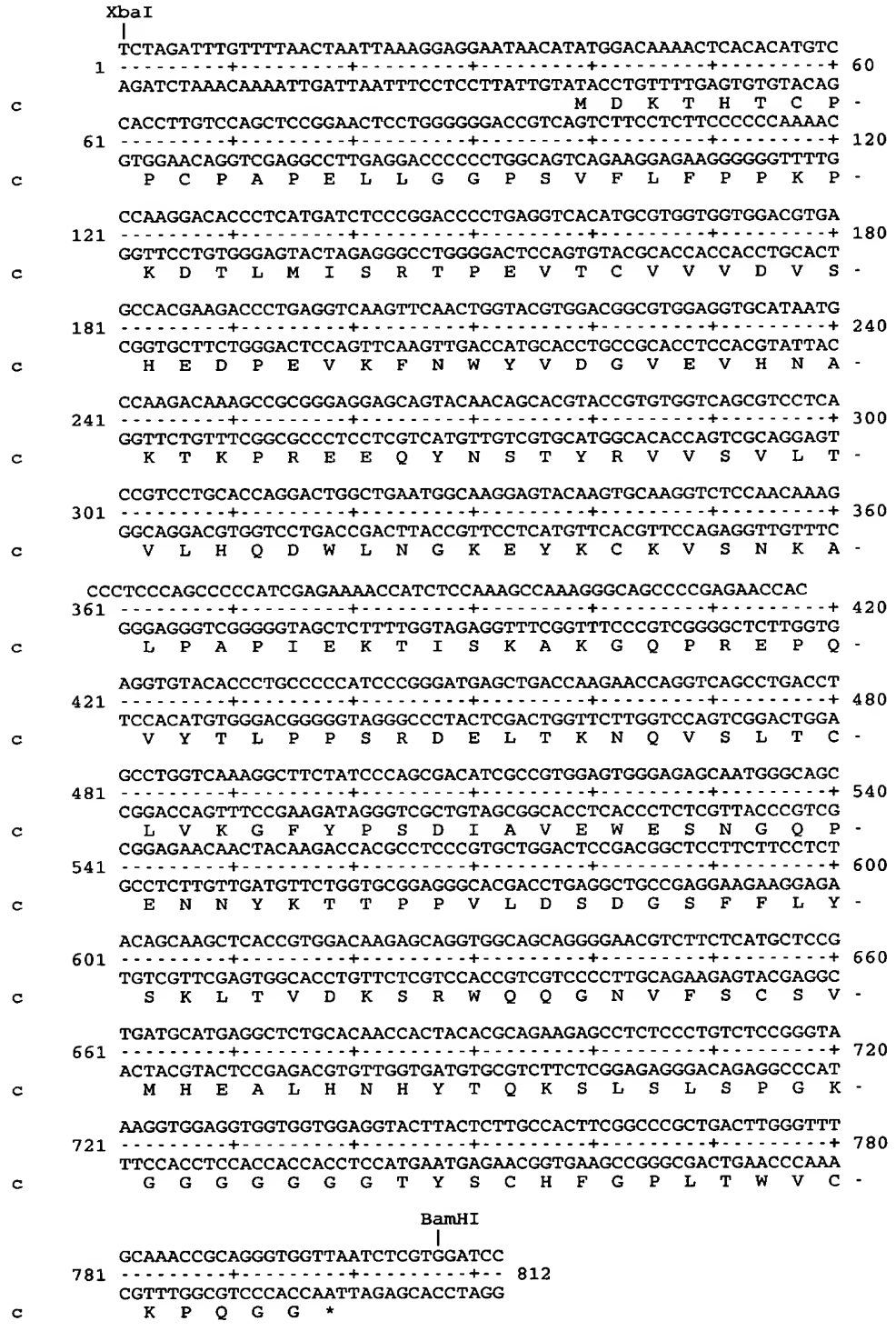
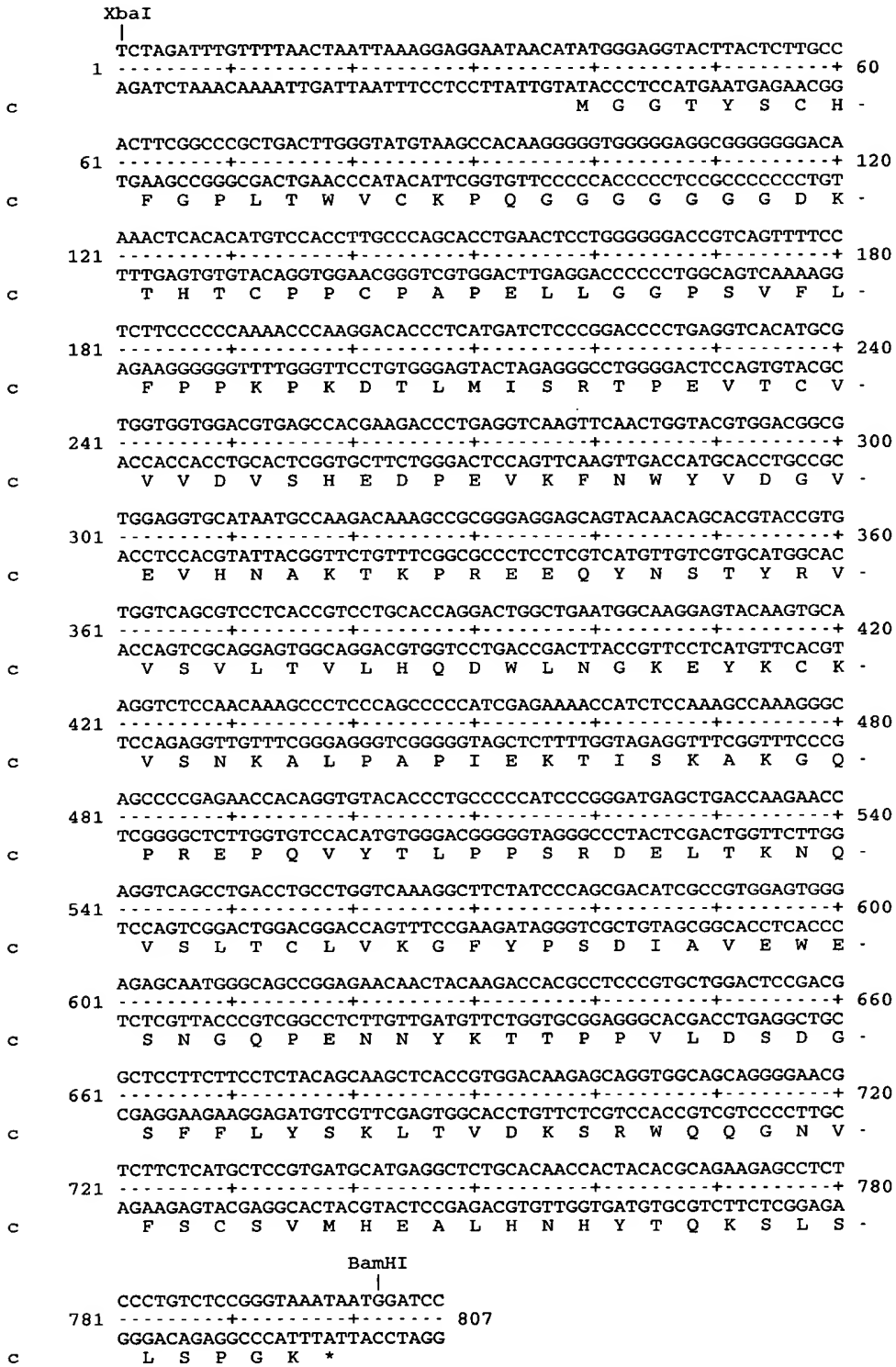


FIGURE 14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F G P L T W V C K P Q G G G G G G G G D K
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TTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAAAAGG
T H T C P P C P A P E L L G G P S V F L
TCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCG
AGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGC
F P P K P K D T L M I S R T P E V T C V
TGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG
ACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGC
V V D V S H E D P E V K F N W Y V D G V
TGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG
ACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCAC
E V H N A K T K P R E E Q Y N S T Y R V
TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCA
ACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGT
V S V L T V L H Q D W L N G K E Y K C K
AGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGC
TCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCG
V S N K A L P A P I E K T I S K A K G Q
AGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACC
TCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGG
P R E P Q V Y T L P P S R D E L T K N Q
AGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
TCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCC
V S L T C L V K G F Y P S D I A V E W E
AGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACG
TCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGC
S N G Q P E N N Y K T T P P V L D S D G
GCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACG
CGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGC
S F F L Y S K L T V D K S R W Q Q G N V
TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT
AGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGA
F S C S V M H E A L H N H Y T Q K S L S
BamHI
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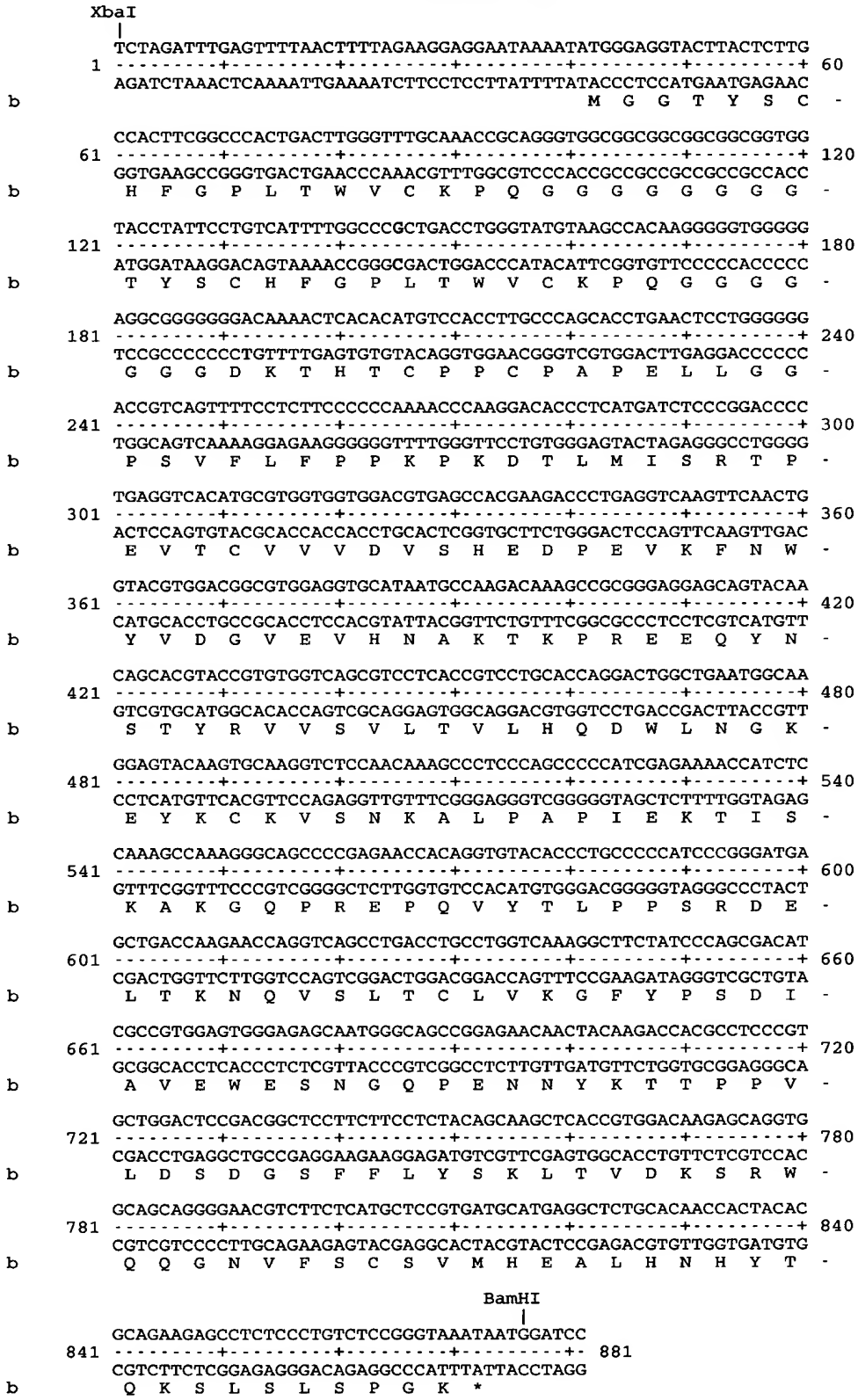
GGGACAGAGGCCCATTTATTACCTAGG
L S P G K *

FIGURE 15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AGATCTAAACTCAAAATTGAAAATCTTCCTCCTTATTTTATACCCTCCATGAATGAGAAC
M G G T Y S C
CCACTTCGGCCCACTGACTTGGGTTTGCAAACCGCAGGGTGGCGGCGGCGGCGGCGGTGG
GGTGAAGCCGGGTGACTGAACCCAAACGTTTGGCGTCCCACCGCCGCCGCCGCCGCCACC
H F G P L T W V C K P Q G G G G G G G G
TACCTATTCCTGTCATTTTGGCCCGCTGACCTGGGTATGTAAGCCACAAGGGGGTGGGGG
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T Y S C H F G P L T W V C K P Q G G G G
AGGCGGGGGGGACAAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGG
TCCGCCCCCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCC
G G G D K T H T C P P C P A P E L L G G
ACCGTCAGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCC
TGGCAGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGG
P S V F L F P P K P K D T L M I S R T P
TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTG
ACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGAC
E V T C V V V D V S H E D P E V K F N W
GTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAA
CATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTT
Y V D G V E V H N A K T K P R E E Q Y N
CAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAA
GTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTT
S T Y R V V S V L T V L H Q D W L N G K
GGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC
CCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAG
E Y K C K V S N K A L P A P I E K T I S
CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGA
GTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACT
K A K G Q P R E P Q V Y T L P P S R D E
GCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT
CGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTA
L T K N Q V S L T C L V K G F Y P S D I
CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGT
GCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCA
A V E W E S N G Q P E N N Y K T T P P V
GCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTG
CGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCAC
L D S D G S F F L Y S K L T V D K S R W
GCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAC
CGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTG
Q Q G N V F S C S V M H E A L H N H Y T
BamHI
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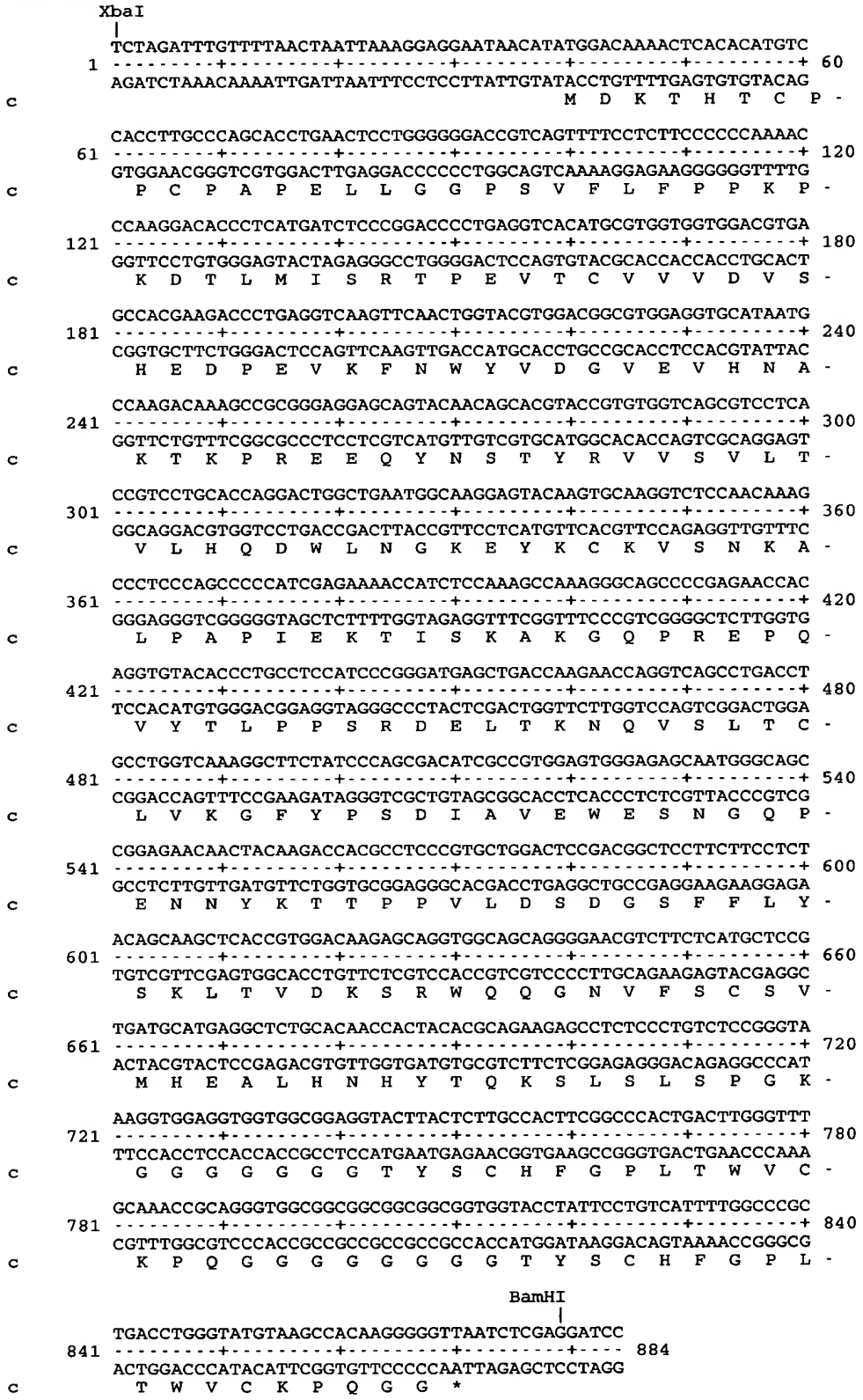
CGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG
Q K S L S L S P G K *

FIGURE 16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AGATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACCTGTTTTGAGTGTGTACAG
M D K T H T C P
CACCTTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTTTTCCTCTTCCCCCCAAAAC
GTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAAAAGGAGAAGGGGGGTTTTG
P C P A P E L L G G P S V F L F P P K P
CCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA
GGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT
K D T L M I S R T P E V T C V V V D V S
GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
H E D P E V K F N W Y V D G V E V H N A
CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCA
GGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT
K T K P R E E Q Y N S T Y R V V S V L T
CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
GGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTC
V L H Q D W L N G K E Y K C K V S N K A
CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC
GGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG
L P A P I E K T I S K A K G Q P R E P Q
AGGTGTACACCCTGCCTCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT
TCCACATGTGGGACGGAGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGA
V Y T L P P S R D E L T K N Q V S L T C
GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCG
L V K G F Y P S D I A V E W E S N G Q P
CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCT
GCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGA
E N N Y K T T P P V L D S D G S F F L Y
ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG
TGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC
S K L T V D K S R W Q Q G N V F S C S V
TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA
ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT
M H E A L H N H Y T Q K S L S L S P G K
AAGGTGGAGGTGGTGGCGGAGGTACTTACTCTTGCCACTTCGGCCCACTGACTTGGGTTT
TTCCACCTCCACCACCGCCTCCATGAATGAGAACGGTGAAGCCGGGTGACTGAACCCAAA
G G G G G G G T Y S C H F G P L T W V C
GCAAACCGCAGGGTGGCGGCGGCGGCGGCGGTGGTACCTATTCCTGTCATTTTGGCCCGC
CGTTTGGCGTCCCACCGCCGCCGCCGCCGCCACCATGGATAAGGACAGTAAAACCGGGCG
K P Q G G G G G G G G T Y S C H F G P L
BamHI
TGACCTGGGTATGTAAGCCACAAGGGGGTTAATCTCGAGGATCC
ACTGGACCCATACATTCGGTGTTCCCCCAATTAGAGCTCCTAGG
T W V C K P Q G G *

FIGURE 17A


[AatII sticky end]
(position #4358 in pAMG21)
5' GCGTAACGTATGCATGGTCTCC-
3' TGCACGCATTGCATACGTACCAGAGG-
-CCATGCGAGAGTAGGGAACTGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACT-
-GGTACGCTCTCATCCCTTGACGGTCCGTAGTTTATTTTGCTTTCCGAGTCAGCTTTCTGA-
-GGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCCTGAGTAGGACAAATCCGC-
-CCCGGAAAGCAAAATAGACAACAAACAGCCACTTGCGAGAGGACTCATCCTGTTTAGGCG-
-CGGGAGCGGATTTGAACGTTGCGAAGCAACGGCCCGGAGGGTGGCGGGCAGGACGCCCGC-
-GCCCTCGCCTAAACTTGCAACGCTTCGTTGCCGGGCCTCCCACCGCCCGTCCTGCGGGCG-
-CATAAACTGCCAGGCATCAAATTAAGCAGAAGGCCATCCTGACGGATGGCCTTTTTGCGT-
-GTATTTGACGGTCCGTAGTTTAATTCGTCTTCCGGTAGGACTGCCTACCGGAAAAACGCA-
AatII
-TTCTACAAACTCTTTTGTTTATTTTTCTAAATACATTCAAATATGGACGTCGTACTTAAC-
-AAGATGTTTGAGAAAACAAATAAAAAGATTTATGTAAGTTTATACCTGCAGCATGAATTG-
-TTTTAAAGTATGGGCAATCAATTGCTCCTGTTAAAATTGCTTTAGAAATACTTTGGCAGC-
-AAAATTTCATACCCGTTAGTTAACGAGGACAATTTTAACGAAATCTTTATGAAACCGTCG-
-GGTTTGTTGTATTGAGTTTCATTTGCGCATTGGTTAAATGGAAAGTGACCGTGCGCTTAC-
-CCAAACAACATAACTCAAAGTAAACGCGTAACCAATTTACCTTTCACTGGCACGCGAATG-
-TACAGCCTAATATTTTTGAAATATCCCAAGAGCTTTTTCCTTCGCATGCCCACGCTAAAC-
-ATGTCGGATTATAAAAACTTTATAGGGTTCTCGAAAAAGGAAGCGTACGGGTGCGATTTG-
-ATTCTTTTTCTCTTTTGGTTAAATCGTTGTTTGATTTATTATTTGCTATATTTATTTTTC-
-TAAGAAAAAGAGAAAACCAATTTAGCAACAAACTAAATAATAAACGATATAAATAAAAAG-
-GATAATTATCAACTAGAGAAGGAACAATTAATGGTATGTTCATACACGCATGTAAAAATA-
-CTATTAATAGTTGATCTCTTCCTTGTTAATTACCATACAAGTATGTGCGTACATTTTTAT-
-AACTATCTATATAGTTGTCTTTCTCTGAATGTGCAAAACTAAGCATTCCGAAGCCATTAT-
-TTGATAGATATATCAACAGAAAGAGACTTACACGTTTTGATTCGTAAGGCTTCGGTAATA-
-TAGCAGTATGAATAGGGAAACTAAACCCAGTGATAAGACCTGATGATTTCGCTTCTTTAA-
-ATCGTCATACTTATCCCTTTGATTTGGGTCACTATTCTGGACTACTAAAGCGAAGAAATT-
-TTACATTTGGAGATTTTTTATTTACAGCATTGTTTTCAAATATATTCCAATTAATCGGTG-
-AATGTAAACCTCTAAAAAATAAATGTCGTAACAAAAGTTTATATAAGGTTAATTAGCCAC-
-AATGATTGGAGTTAGAATAATCTACTATAGGATCATATTTTATTAAATTAGCGTCATCAT-
-TTACTAACCTCAATCTTATTAGATGATATCCTAGTATAAAATAATTTAATCGCAGTAGTA-
-AATATTGCCTCCATTTTTTAGGGTAATTATCCAGAATTGAAATATCAGATTTAACCATAG-
-TTATAACGGAGGTAAAAAATCCCATTAATAGGTCTTAACTTTATAGTCTAAATTGGTATC-
-AATGAGGATAAATGATCGCGAGTAAATAATATTCACAATGTACCATTTTAGTCATATCAG-
-TTACTCCTATTTACTAGCGCTCATTTATTATAAGTGTTACATGGTAAAATCAGTATAGTC-
-ATAAGCATTGATTAATATCATTATTGCTTCTACAGGCTTTAATTTTATTAATTATTCTGT-
-TATTCGTAACTAATTATAGTAATAACGAAGATGTCCGAAATTAAAATAATTAATAAGACA-
-AAGTGTCGTCGGCATTTATGTCTTTCATACCCATCTCTTTATCCTTACCTATTGTTTGTC-
-TTCACAGCAGCCGTAAATACAGAAAGTATGGGTAGAGAAATAGGAATGGATAACAAACAG-
-GCAAGTTTTGCGTGTTATATATCATTAAAACGGTAATAGATTGACATTTGATTCTAATAA-
-CGTTCAAAACGCACAATATATAGTAATTTTGCCATTATCTAACTGTAAACTAAGATTATT-

FIGURE 17B

```
-ATTGGATTTTTGTCACACTATTATATCGCTTGAAATACAATTGTTTAACATAAGTACCTG-
-TAACCTAAAAACAGTGTGATAATATAGCGAACTTTATGTTAACAAATTGTATTCATGGAC-

-TAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTTATAGTCGATTAATCGATTTGATT-
-ATCCTAGCATGTCCAAATGCGTTCTTTTACCAAACAATATCAGCTAATTAGCTAAACTAA-

-CTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGA-
-GATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACCAATTGCGCAACCTTAAGCT-

                                                 SacII
-GCTCACTAGTGTCGACCTGCAGGGTACCATGGAAGCTTACTCGAGGATCCGCGGAAAGAA-
-CGAGTGATCACAGCTGGACGTCCCATGGTACCTTCGAATGAGCTCCTAGGCGCCTTTCTT-

-GAAGAAGAAGAAGAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATA-
-CTTCTTCTTCTTCTTTCGGGCTTTCCTTCGACTCAACCGACGACGGTGGCGACTCGTTAT-

-ACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTGCTGAAAGGAGG-
-TGATCGTATTGGGGAACCCCGGAGATTTGCCCAGAACTCCCCAAAAAACGACTTTCCTCC-

-AACCGCTCTTCACGCTCTTCACGC 3'          [SacII sticky end]
-TTGGCGAGAAGTGCGAGAAGTG   5'       (position #5904 in pAMG21)
```

FIGURE 18

Erythroid parameters EMP-Fc, single bolus injection.

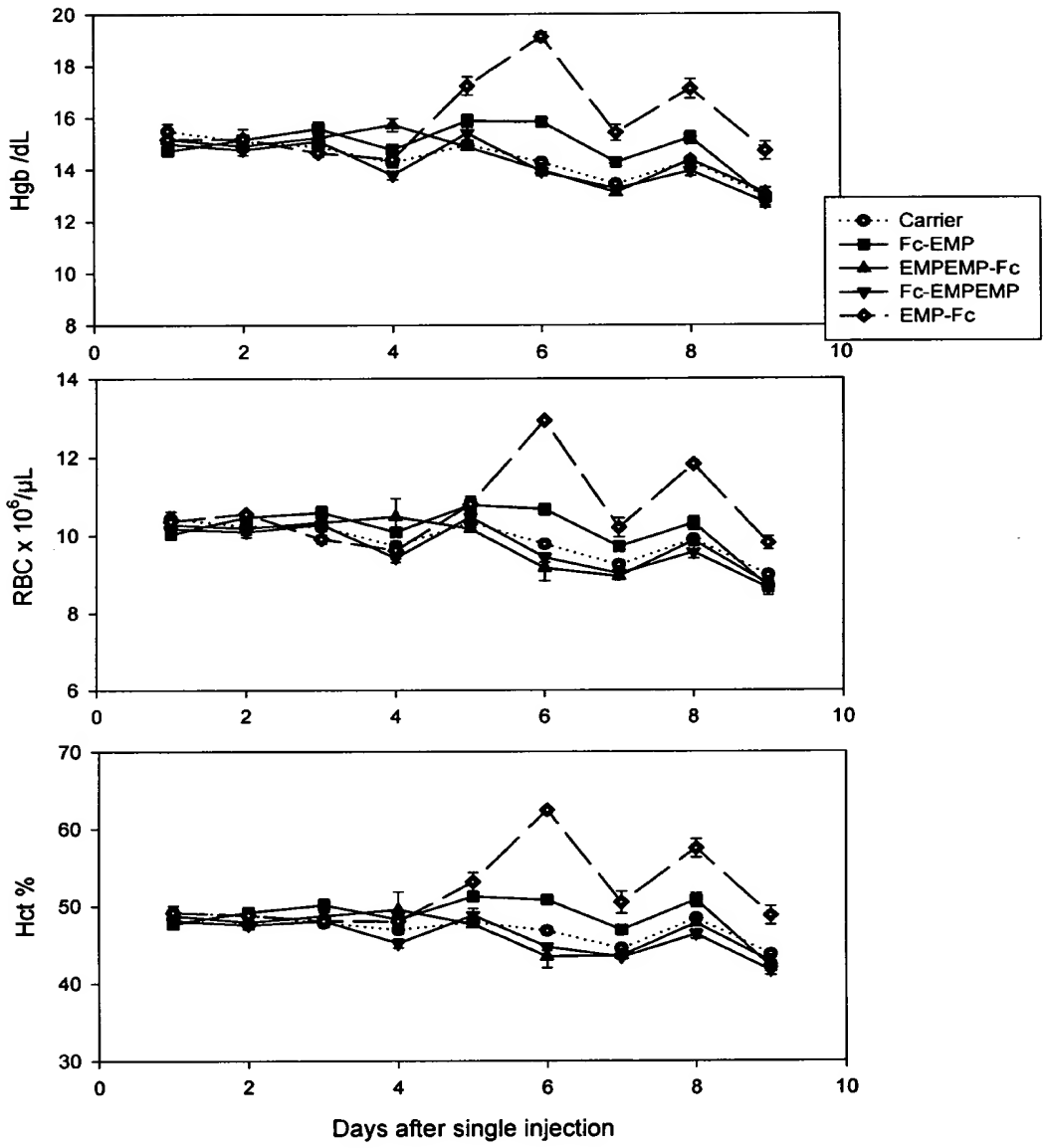


FIGURE 19

Normal female BDF1 mice treated with 100ug/kg EMP-Fc
in 7-day micro osmotic pumps

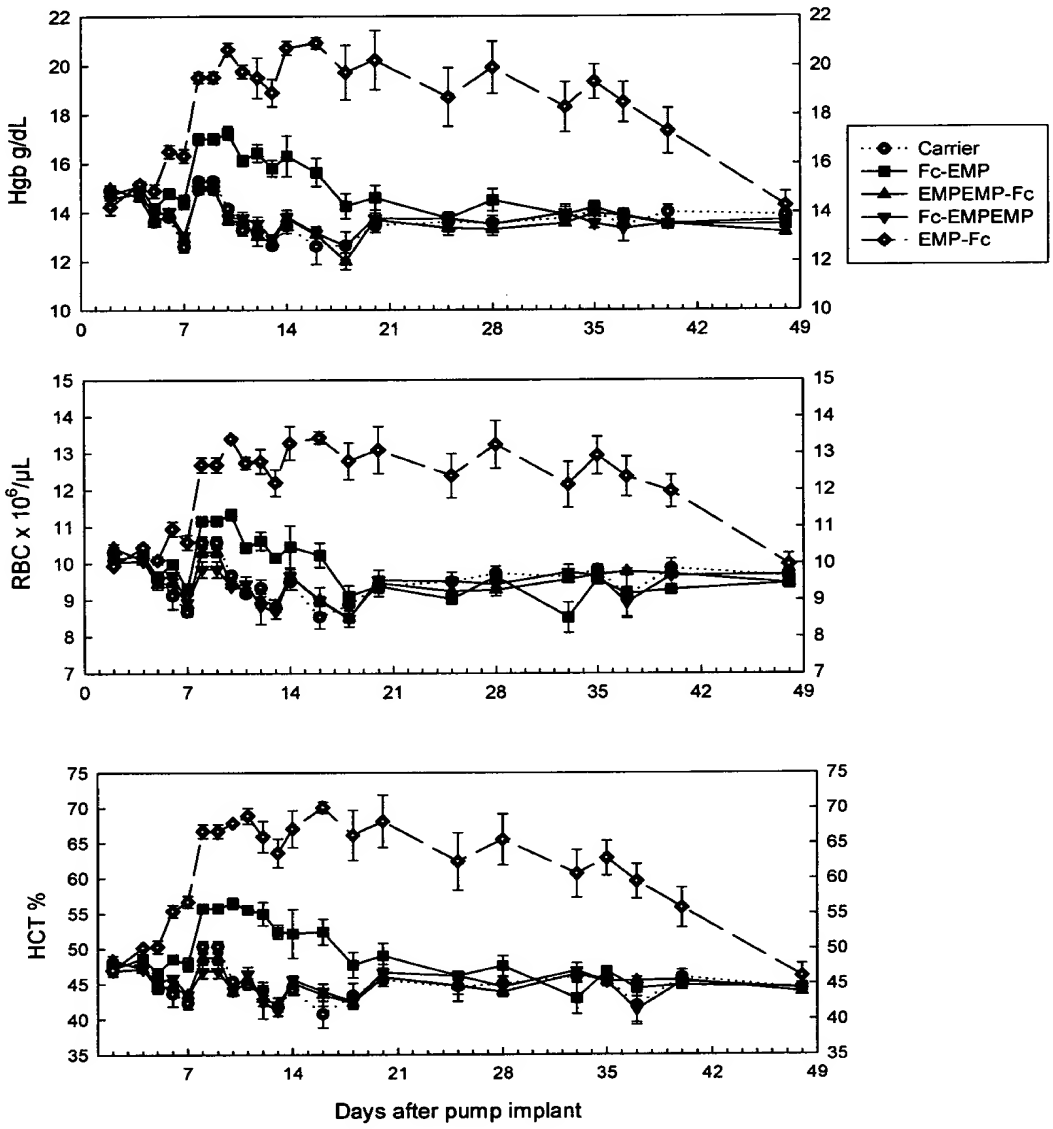
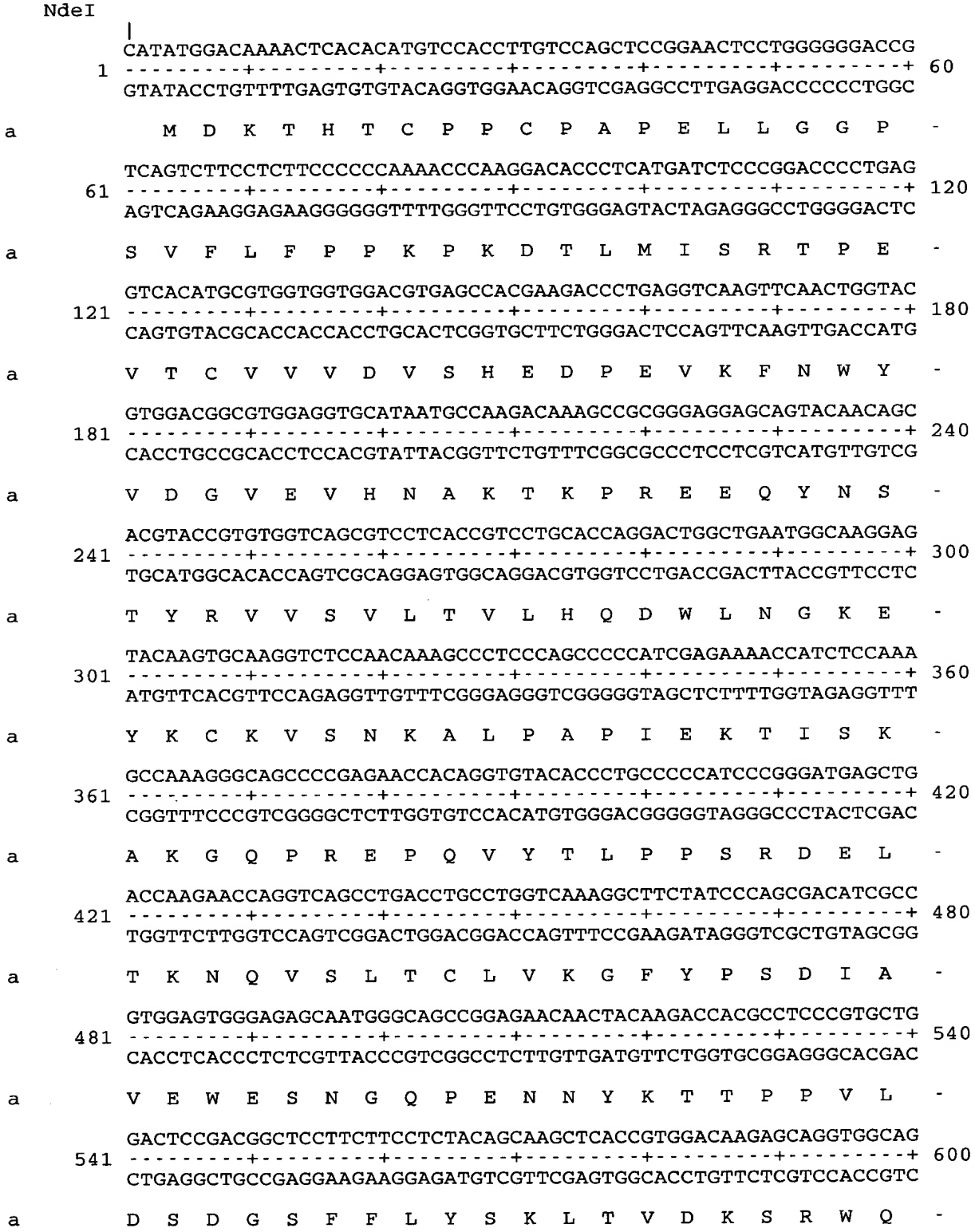


FIGURE 19A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a M D K T H T C P P C P A P E L L G G P -
TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG
a V D G V E V H N A K T K P R E E Q Y N S -
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC
a T Y R V V S V L T V L H Q D W L N G K E -
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG
CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L -
GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
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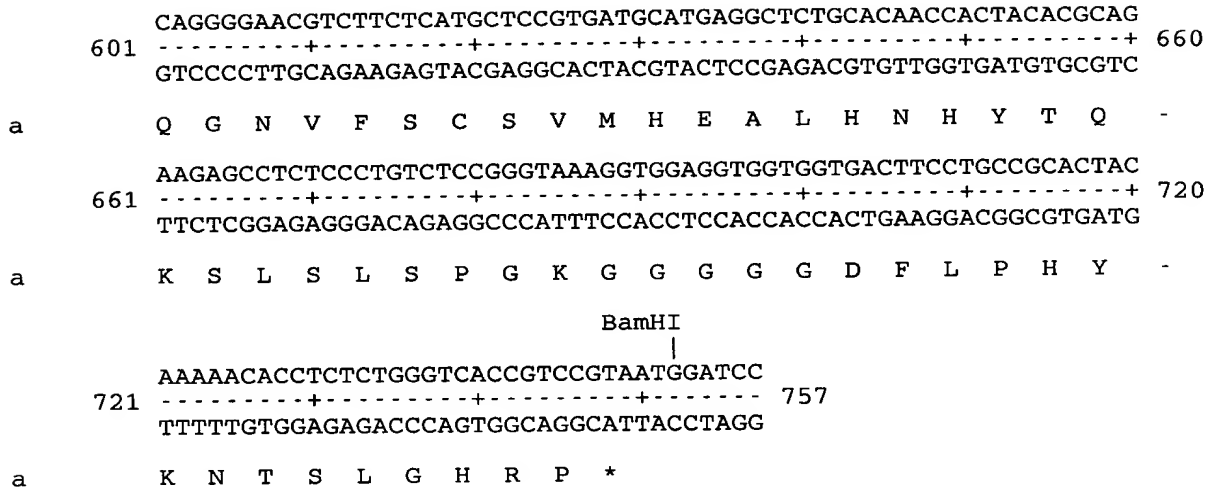
a D S D G S F F L Y S K L T V D K S R W Q -

FIGURE 19B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601
660
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a
Q G N V F S C S V M H E A L H N H Y T Q -
AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTGACTTCCTGCCGCACTAC
661
720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCACTGAAGGACGGCGTGATG
a
K S L S L S P G K G G G G G D F L P H Y -
BamHI
AAAAACACCTCTCTGGGTCACCGTCCGTAATGGATCC
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757
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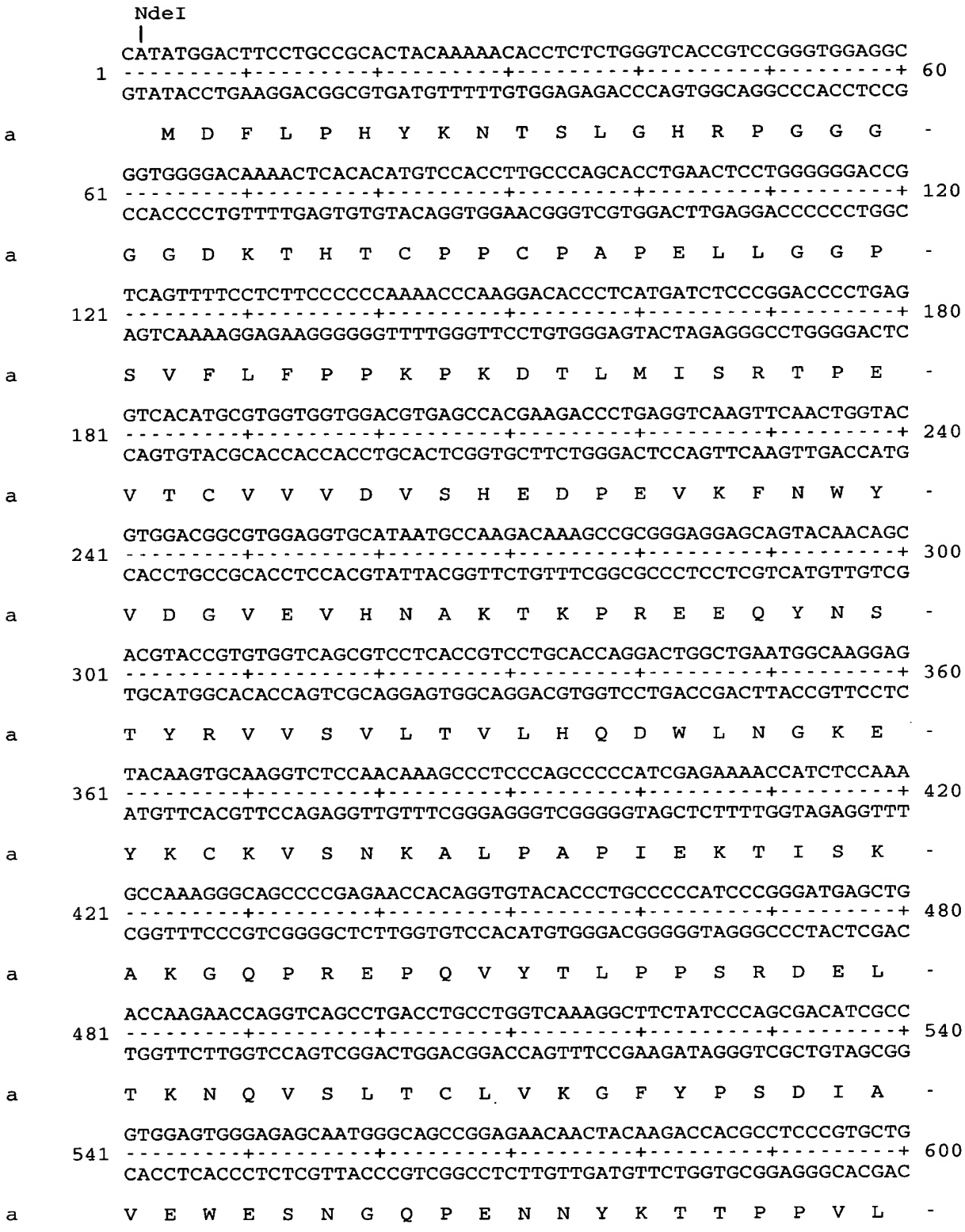
a
K N T S L G H R P *

FIGURE 20A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a M D F L P H Y K N T S L G H R P G G G -
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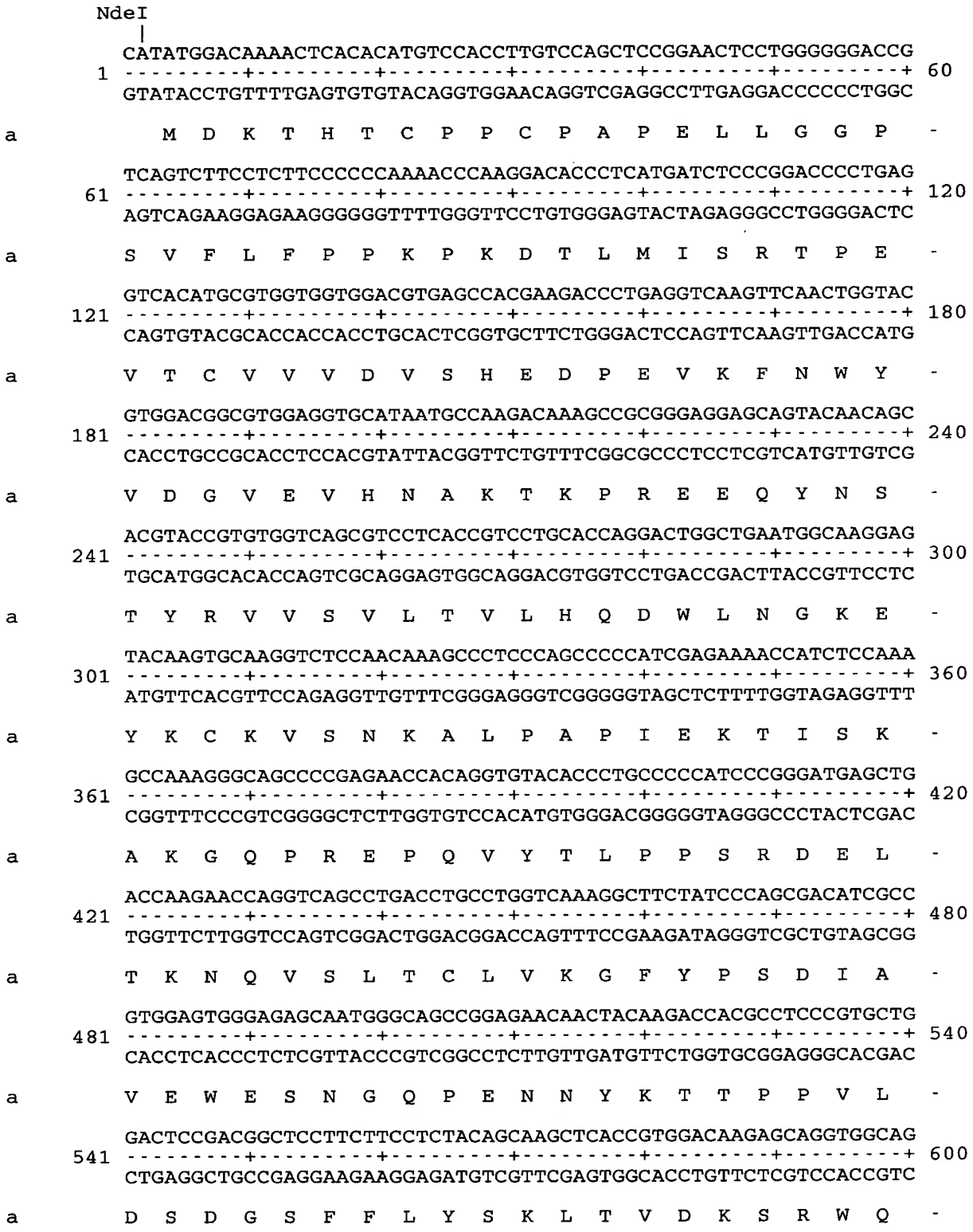
CCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGC
a G G D K T H T C P P C P A P E L L G G P -
TCAGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
AGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG
a V D G V E V H N A K T K P R E E Q Y N S -
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC
a T Y R V V S V L T V L H Q D W L N G K E -
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGGTAGCTCTTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG
CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L -

FIGURE 20B

```
        GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
    601 ---------+---------+---------+---------+---------+---------+ 660
        CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a       D  S  D  G  S  F  F  L  Y  S  K  L  T  V  D  K  S  R  W  Q  -

        CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
    661 ---------+---------+---------+---------+---------+---------+ 720
        GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a       Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  -

                                           BamHI
                                               |
        AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCCGCGG
    721 ---------+---------+---------+---------+- 761
        TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGGCGCC

a       K  S  L  S  L  S  P  G  K  *
```

FIGURE 21A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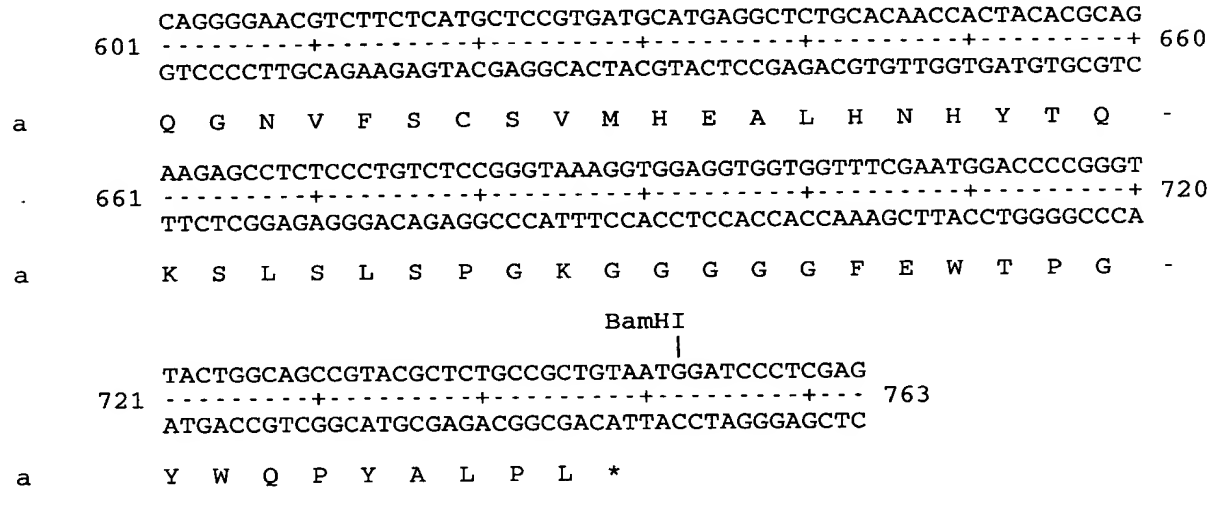
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC
a M D K T H T C P P C P A P E L L G G P -
TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG
a V D G V E V H N A K T K P R E E Q Y N S -
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC
a T Y R V V S V L T V L H Q D W L N G K E -
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGGTAGCTCTTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG
CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L -
GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC
a D S D G S F F L Y S K L T V D K S R W Q -

FIGURE 21B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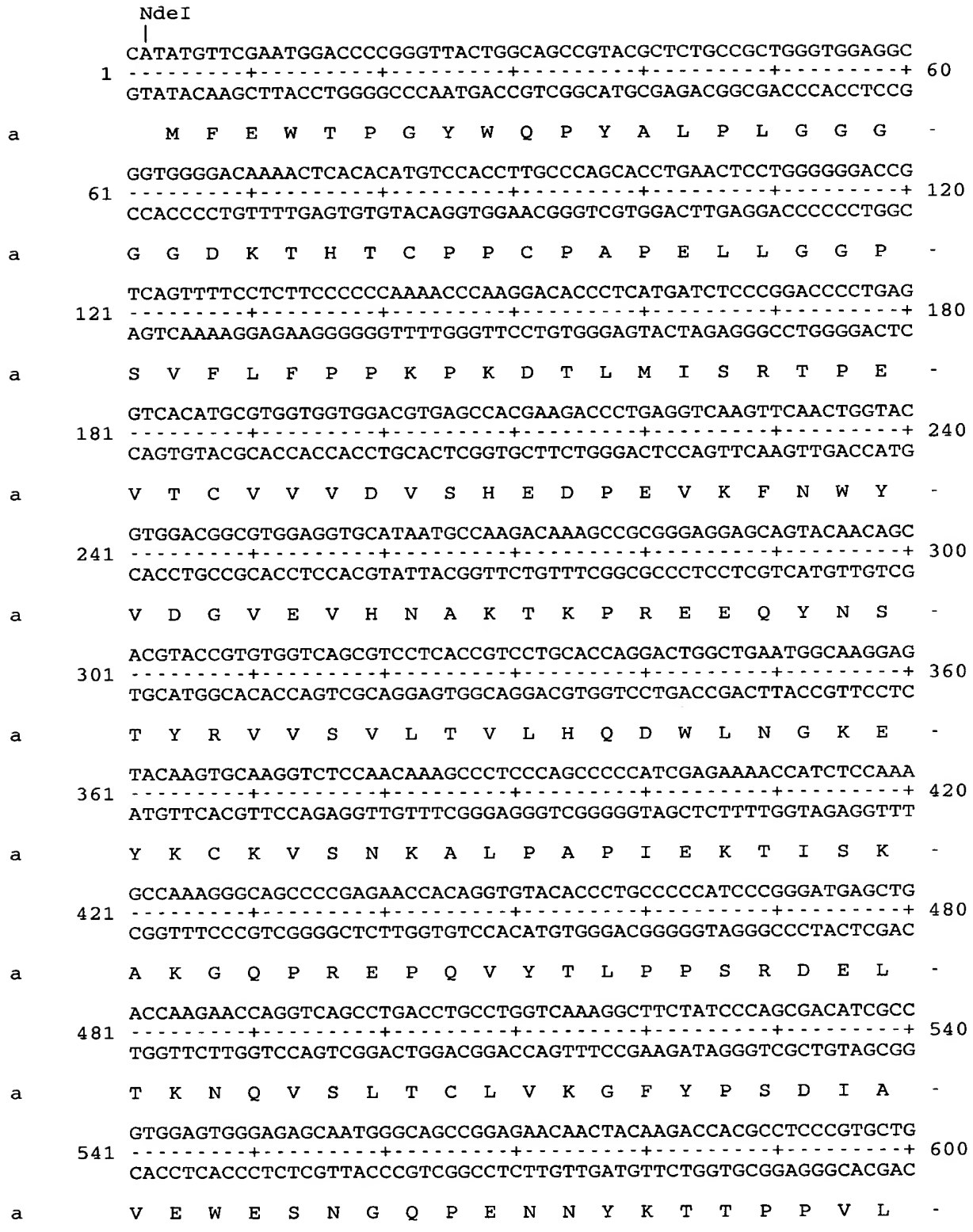
601
660
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
a
Q G N V F S C S V M H E A L H N H Y T Q -
AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTTCGAATGGACCCCGGGT
661
720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAAAGCTTACCTGGGGCCCA
a
K S L S L S P G K G G G G G F E W T P G -
BamHI
TACTGGCAGCCGTACGCTCTGCCGCTGTAATGGATCCCTCGAG
721
763
ATGACCGTCGGCATGCGAGACGGCGACATTACCTAGGGAGCTC
a
Y W Q P Y A L P L *

FIGURE 22A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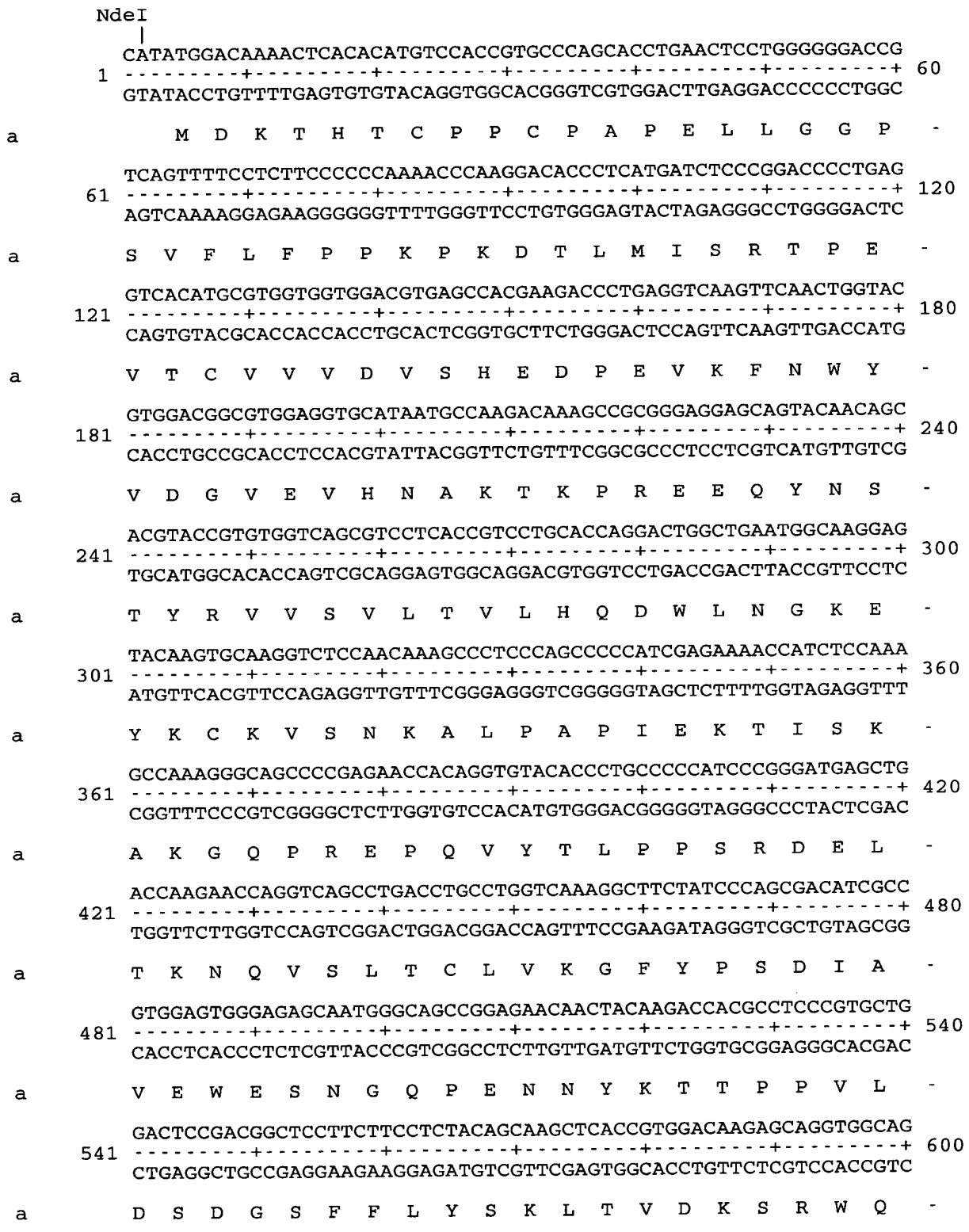
GTATACAAGCTTACCTGGGGCCCAATGACCGTCGGCATGCGAGACGGCGACCCACCTCCG
a M F E W T P G Y W Q P Y A L P L G G G -
GGTGGGGACAAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCG
CCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGC
a G G D K T H T C P P C P A P E L L G G P -
TCAGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
AGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG
a V D G V E V H N A K T K P R E E Q Y N S -
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC
a T Y R V V S V L T V L H Q D W L N G K E -
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG
CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L -

FIGURE 22B

```
     GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
601  ---------+---------+---------+---------+---------+---------+ 660
     CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a        D  S  D  G  S  F  F  L  Y  S  K  L  T  V  D  K  S  R  W  Q   -

     CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
661  ---------+---------+---------+---------+---------+---------+ 720
     GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a        Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q   -

                                    BamHI
                                      |
     AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
721  ---------+---------+---------+------- 757
     TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG

a        K  S  L  S  L  S  P  G  K  *
```

FIGURE 23A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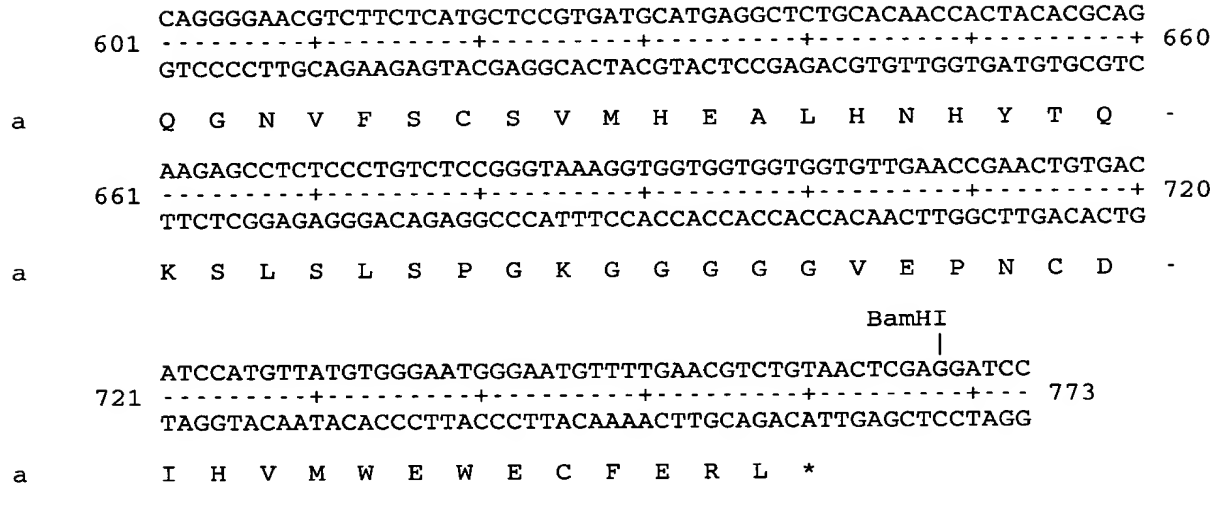
GTATACCTGTTTTGAGTGTGTACAGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGC
a M D K T H T C P P C P A P E L L G G P -
TCAGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
AGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG
a V D G V E V H N A K T K P R E E Q Y N S -
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC
a T Y R V V S V L T V L H Q D W L N G K E -
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG
CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L -
GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC
a D S D G S F F L Y S K L T V D K S R W Q -
1
61
121
181
241
301
361
421
481
541
60
120
180
240
300
360
420
480
540
600

FIGURE 23B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660
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a
Q G N V F S C S V M H E A L H N H Y T Q -
AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGTGGTGGTGGTGTTGAACCGAACTGTGAC
661
720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCACCACCACCACAACTTGGCTTGACACTG
a
K S L S L S P G K G G G G G V E P N C D -
BamHI
ATCCATGTTATGTGGGAATGGGAATGTTTTGAACGTCTGTAACTCGAGGATCC
721
773
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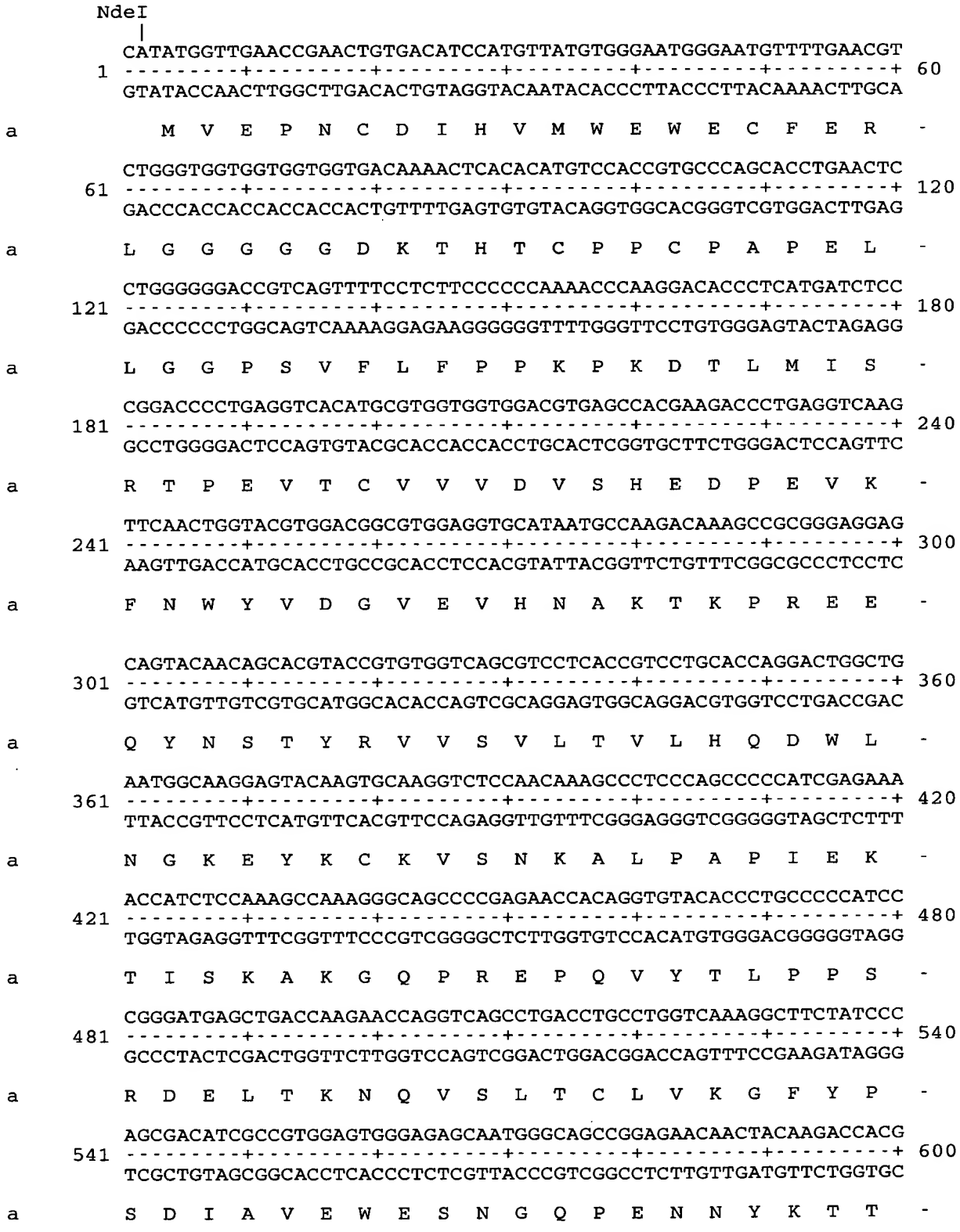
a
I H V M W E W E C F E R L *

FIGURE 24A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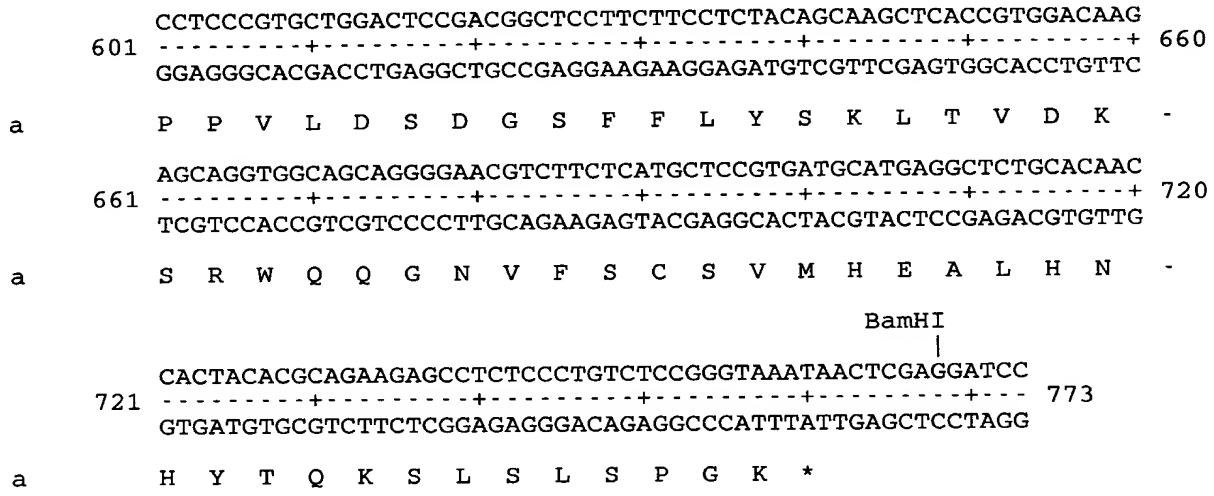
a M V E P N C D I H V M W E W E C F E R -
CTGGGTGGTGGTGGTGGTGACAAAACTCACACATGTCCACCGTGCCCAGCACCTGAACTC
GACCCACCACCACCACCACTGTTTTGAGTGTGTACAGGTGGCACGGGTCGTGGACTTGAG
a L G G G G G D K T H T C P P C P A P E L -
CTGGGGGGACCGTCAGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCC
GACCCCCCTGGCAGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGG
a L G G P S V F L F P P K P K D T L M I S -
CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG
GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC
a R T P E V T C V V V D V S H E D P E V K -
TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG
AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC
a F N W Y V D G V E V H N A K T K P R E E -
CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
GTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGAC
a Q Y N S T Y R V V S V L T V L H Q D W L -
AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA
TTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT
a N G K E Y K C K V S N K A L P A P I E K -
ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC
TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG
a T I S K A K G Q P R E P Q V Y T L P P S -
CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
GCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGG
a R D E L T K N Q V S L T C L V K G F Y P -
AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACG
TCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGC
a S D I A V E W E S N G Q P E N N Y K T T -

FIGURE 24B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660
GGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTC
a
P P V L D S D G S F F L Y S K L T V D K -
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC
661
720
TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG
a
S R W Q Q G N V F S C S V M H E A L H N -
BamHI
CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAACTCGAGGATCC
721
773
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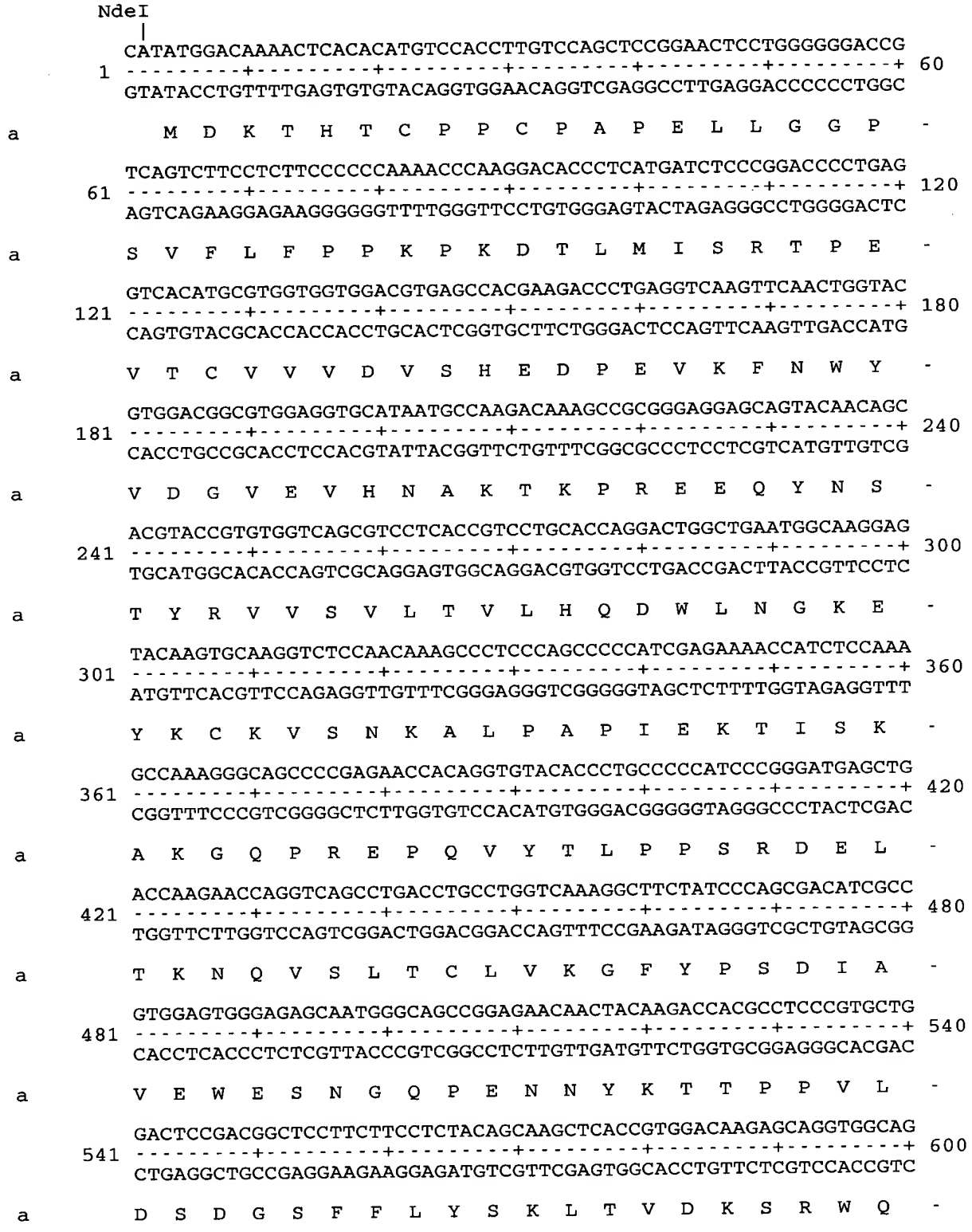
a
H Y T Q K S L S L S P G K *

FIGURE 25A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GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC
a M D K T H T C P P C P A P E L L G G P -
TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a S V F L F P P K P K D T L M I S R T P E -
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a V T C V V V D V S H E D P E V K F N W Y -
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG
a V D G V E V H N A K T K P R E E Q Y N S -
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC
a T Y R V V S V L T V L H Q D W L N G K E -
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
a Y K C K V S N K A L P A P I E K T I S K -
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a A K G Q P R E P Q V Y T L P P S R D E L -
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a T K N Q V S L T C L V K G F Y P S D I A -
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG
CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC
a V E W E S N G Q P E N N Y K T T P P V L -
GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
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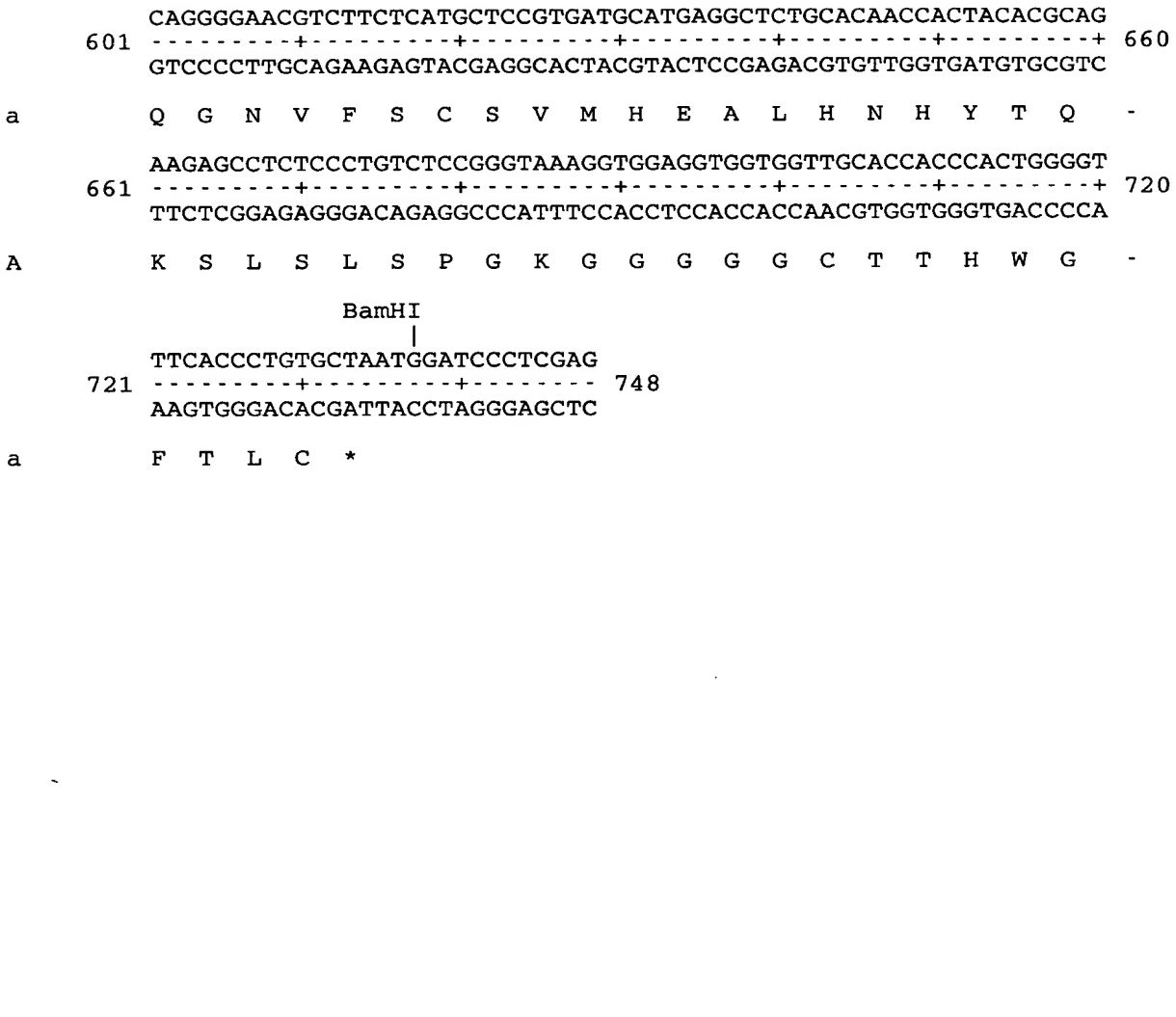
a D S D G S F F L Y S K L T V D K S R W Q -

FIGURE 25B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a Q G N V F S C S V M H E A L H N H Y T Q -
AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTGCACCACCCACTGGGGT
661 ---------+---------+---------+---------+---------+---------+ 720
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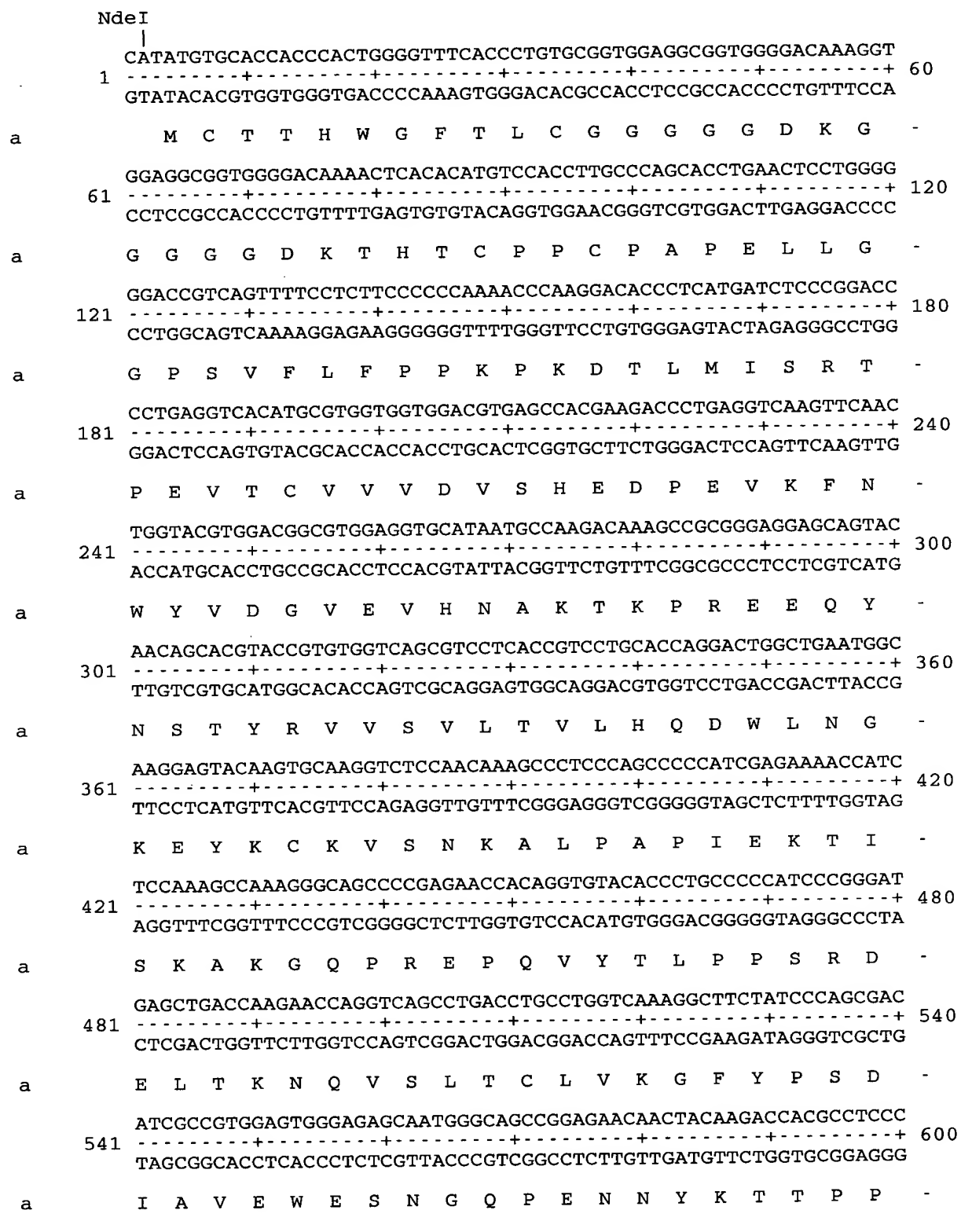
A K S L S L S P G K G G G G G C T T H W G -
BamHI
TTCACCCTGTGCTAATGGATCCCTCGAG
721 ---------+---------+-------- 748
AAGTGGGACACGATTACCTAGGGAGCTC
a F T L C *

FIGURE 26A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CCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCC
a G G G G D K T H T C P P C P A P E L L G -
GGACCGTCAGTTTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACC
CCTGGCAGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGG
a G P S V F L F P P K P K D T L M I S R T -
CCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
GGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTG
a P E V T C V V V D V S H E D P E V K F N -
TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTAC
ACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATG
a W Y V D G V E V H N A K T K P R E E Q Y -
AACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGC
TTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCG
a N S T Y R V V S V L T V L H Q D W L N G -
AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
TTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAG
a K E Y K C K V S N K A L P A P I E K T I -
TCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAT
AGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTA
a S K A K G Q P R E P Q V Y T L P P S R D -
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CTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTG
a E L T K N Q V S L T C L V K G F Y P S D -
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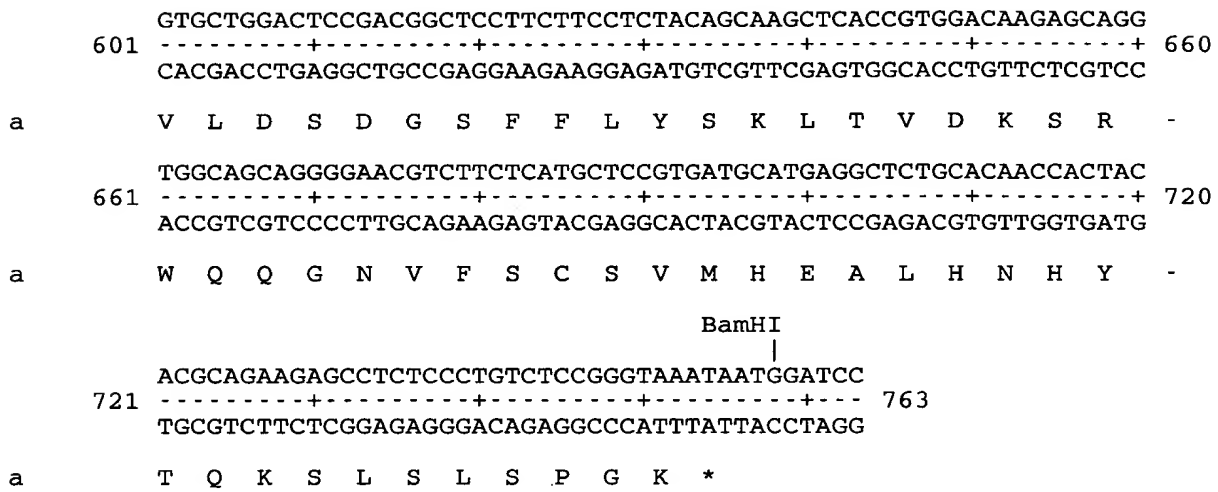
a I A V E W E S N G Q P E N N Y K T T P P -

FIGURE 26B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a V L D S D G S F F L Y S K L T V D K S R -
TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
661 720
ACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATG
a W Q Q G N V F S C S V M H E A L H N H Y -
BamHI
ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
721 763
TGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG
a T Q K S L S L S P G K *